Homo sapi Human DNA

AX300942 Sequence
BX49247 Sebrafish
AC120369 Mus muscu
AC13066 Mus muscu
AC031366 Mus muscu
AC087504 Homo sapi
AC021336 Homo sapi
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AC020334 Homo sapi
AC097363 Rattus no
AC099248 Rattus no
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AC09248 Homo sapi
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AC148631 Callithri
AC009306 Homo sapi
AR15176 Sequence
AX972010 Sequence
AX972010 Sequence
AX121878 Human DNA
AL121878 Human DNA

Perfect score:

Sequence:

Searched:

Database

OM nucleic

Run on:

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Roesl, F., Soto, U., Coy, J., Finzer, P., Delius, H., Poustka, A., zur Hausen, H. and Patzelt, A. Regulatory sequences of the human mcp-1 gene Patent: EP 1170372-A 1 09-JAN-2002; DEDTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OBFFENTLICHEN RECHTS (DE)
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100.0%; Pred. No. 1.7e-142;
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BD110729
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AC123884
AC012469
AL359183
AX300942
BX649247
AC120369
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Best Local Similarity 100.
Matches 600; Conservative
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7.0 194946
7.0 210525
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6.9 158016
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ALG26807 MOUSE DNA
AL713839 MUS WUSCU
ACC73824 MUS WUSCU
ACC73824 MUS WUSCU
ACL28200 Rattus no
ACL29672 Rattus no
ACC95987 Rattus no
ACC95987 Rattus no
ACC96469 Rattus no
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AF519531 Homo sapi
Y18933 Homo sapien
AC005549 Homo sapien
X60001 H.sapiens 9
AC123203 Rattus no
AC114440 Rattus no
AC16494 Sequence 14
AC022299 Mus muscu
                                                                        August 3, 2005, 21:53:02 ; Search time 2411.66 Seconds (without alignments) 12055.236 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                     4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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AL626807
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PAT 01-FEB-2002

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Gaps

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Result Š.

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variation	variation variation repeat_region variation variation gene mRNA
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1041 GTTTCCCTCCATACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 7100
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Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 9.4e-143;
Matches 600; Conservative 0; Mismatches 0; Indels
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Homo sapiens MCP-1 gene and enhancer region.
Y18933
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MCP-1 gene; monocyte chemoattractant protein-1.
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In Unpublished

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In Unpublished

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

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Ye, W. J., Zhao, J. and Zody, M.

Direct Submission

AL Submitted (27-AUG-1998) Whitehead Institute/MIT Center for Genome stearch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 120 Charles Street, Cambridge, MA 02141, USA

Boutwell, C., Brown, A., Castle, A., Collymore, A., Gerraigery, K., Grant, G., Gollins, S., Collymore, A., Goody, B., Corliss, D., Depayre, E.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC005549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
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1 (bases 1 to 14716)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.215_E_13
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                                                                                                                                                                                                                                                                                                                                                                                                                                   541 GITTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA
                                                                                                                                                                         GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAAGAGGCAGCAATGAAGAATG
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                                                                                                   2 (bases 1 to 11793)
Roeal, F.
Direct Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Newenheimer Feld 506, 69120
Heidelberg, FRG
non-tumorigenic HPV 18 positive cells: the role of the chromatin
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100.0%; Pred. No. 8.9e-143;
ive 0; Mismatches 0;
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Oncogene 19 (29), 3235-3244 (2000)
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complement (27814. .27%
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Direct Submission

Submitted (12-SRP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Dases 1 to 147416)

B irren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collymore, A., Cooke, P., Corliss, D., Depayre, B., Benn, J., Bovon, K., Dewar K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagoes, B., Haedrod, A., Herena, L., Horton, L., Howland, J. C., Jones, C., Kann, L., Kartass, A., Lehoczky, J., Macdorald, P., Marquis, N., McEwan, P., McGurim, X., Marquis, N., McMan, P., McGurim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Raylin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J. and Zody, M., Mheeler, J., Wu, X., Wyman, D., Ye, W.J., Zhao, J. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (122-5EP-1998) Whitehead Institute/MIT Center for Genome Submitted (122-5EP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliav, M., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WIGGR project 1228). The first 2Kb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
1. 147416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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complement (5941. .6051)
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6406. .6455
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ug-09-899-276c-1.rge

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Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

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Biswalo, K., Blair, J., Blankehburg, K., Blyth, P., Brown, M.,

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Charder, K., Cavazos, I., Chen, R., Chen, Y., Chen, Y., Chen, Y.,

Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Daylla, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Dinn, H., Durbin, K., Duval, B., Eaves, K.,

Bran, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Porbes, L., Foster, M., Poster, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC123203 242335 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-28P9, WORKING DRAFT SEQUENCE.
AC123203
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2183 TAGAAATGGTGATGATGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATT 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
Direct Submission S. Schwarz, Albert Einstein College of Submitted (16-MAY-1991) E. Schwarz, Albert Einstein College of Medicine, Dept of Microbiology & Immunology, Forchheimer Bldg Room 411, 1300 Morris Park Avenue, Bronx NY 10461, USA
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Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 121; Conservative 0; Mismatches 0; Indels
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                               1. .2243
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                                                                                                                                                                                                                                                               1 TAGGAAATTTATAGGATCATTAAGAAAGGAGGAAGGAAGAGGAGGAAGTAGCTGGAAG
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H.sapiens gene for JE protein, exons 3 and 4.
                                                                                                                                                                                             ; Score 600; DB 9; L
; Pred. No. 5.3e-143;
0; Mismatches 0;
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complement (48165. .48209)
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JE protein; secretory protein.
Homo sapiens (human)
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ilarity 100.0%;
Conservative 0;
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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gabragoorgis, B., Geer K., Gill, R., Grady, M., Guerra, W., Guevara, Gunzarane, P., Haaland, W., Hamilton, K., Harvard, R., Hardare, J., Hadlan, S.L., Handeron, N., Hernandez, J., Harnandez, J., Hollins, B., Handers, S., Hladdun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladdun, S.L., Hodgson, J., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kelly, S., Kally, S., Kally, J., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Kally, S., Kally, L., Kovar, C., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mandouw, B., Martinez, E., Mandouw, B., Matin, R., Martinez, E., Mandouw, B., Machol, M., Martinez, E., Mandouw, B., Macho, M., Martinez, E., Mandouw, B., Macho, M., Martinez, E., Mandouw, B., Macho, M., Martinez, E., Mandouw, B., Martinez, B., Martinez, E., Poindexter, A., Popovic, D., Primus, B., Pui, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Nei, F., Poindexter, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvattsbeyn, A., Saeson, Saeso
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The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.fmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Rat Genome Sequencing Consortium.
Direct Submission
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188951 AAAAAAACAGAAGCATTAAGAAA--ACAAAGGTGGGGGGGAATTATCCAAAGGTAGA 189008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189009 AATGAAGATGGTGTGTATGTCAAAGGGGGAAGA------GAATCTATG 189050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC114440 245808 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-121P3, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
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Consensus quality: 238611 bases at least Q30 Consensus quality: 239758 bases at least Q30 Estimated insert size: 245041; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 TTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-28P9"
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/note="wgs_end_extension
clone_end:Sp6"
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/note="clone boundary
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Best Local Similarity 57.0%;
Matches 203; Conservative
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                                                                                                                                                                               RS MARZYD, MARIE, METERIAN, LEE., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Anguisher, D., Barder, M., Badon, M., Benamed, F., Baldar, D., Bandaranaike, D., Barder, M., Barnstedd, M., Benamed, F., Baldar, D., Blankenburg, K., Blyth, P., Brown, M., Blair, J., Chan, G., Chen, R., Chen, Y., Chen, Y., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, R., Chen, Y., Chen, S., Chen, G., Chen, R., Chen, R., Chen, T., Chen, G., Chen, R., Chen, Y., Chen, G., Chen, R., Chen, R., Chen, R., Chen, G., Chen, R., Chen, R., Chen, R., Chen, R., Chen, G., Chen, R., Chen, G., Chen, R., Chen, R., Chen, G., Chen, G., Chen, R., Chen, G., Chen, R., C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (109-MAR-2002) Human Genome Sequencing Center, Department Submitted (109-MAR-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (1088es 1 to 245808)

Rat Genome Sequencing Consortium.
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  AC114440.4 GI:25138837
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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GI:25138837
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        VERSION
KEYWORDS
SOURCE
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Center clone name: CRAM.

Center clone name: CRAM.

Assembly program: Phrap; version 0.990329

Assembly program: Phrap; version 0.990329

Consensus quality: 226189 bases at least Q40

Consensus quality: 229460 bases at least Q30

Consensus quality: 229460 bases at least Q20

Estimated insert size: 230674; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Similarity 57.0%; Pred. No. 4.7e-08;
03; Conservative 0; Mismatches 129; Indels
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2 4001: gap of unknown length
12 245808: contig of 241807 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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5719. .7604
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/note="wgs_contig"
1002. .5165
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1. (Dases 1 to leuses).

Shetzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Bursett,C., Chacko,J., Chen,G., Chen,Z.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferragutc,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunartne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., More,D., S., Morgan,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wernsford,G., Zhou,X., Bouck,J., Hodgson,A.,
Wazny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
Direct Subalission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11079355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 160869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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contig of 10158 bp in length
contig of 10158 bp in length
contig of 8324 bp in length
contig of 8324 bp in length
contig of 8002 bp in length
contig of 8002 bp in length
gap of unknown length
contig of 8285 bp in length
contig of 7285 bp in length
contig of 7492 bp in length
contig of 7492 bp in length
contig of 763 bp in length
contig of 753 bp in length
contig of 5923 bp in length
contig of 5923 bp in length
gap of unknown length
contig of 5923 bp in length
contig of 5923 bp in length
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2 (bases 1 to 160869)
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68791:
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Mus musculus clone RP23-433D8, *** SEQUENCING IN PROGRESS ***, 32
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 28-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 TCCAATGA----GGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 CCCACACTATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 TTAGGGTGAAAAGTTACTACTCCACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
                                                                                                                                                      130584 CATCCTGATTACTACATACAAACAGAAAGAGAATAGAGACAAGTGATTGACTGTGGC 130639
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                                                                                                                           301 TAACTTATAGATTTTATACATACAGAGAAATACGGACTAGTGAGAAGCTATTGC 356
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 7218)

Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 70.6; DB 6; Ilarity 3.3%; Pred. No. 1.8e-07; Conservative 237; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 AAGCAAGAGATGATGAAGGCCTAAATATGGA 395
                                                                                                                                                                                                                                                                    7218 bp I
Sequence 14 from patent US 5670367.
I66494.1 GI:2724471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Mus musculus (house mouse)
Mus musculus
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Best Local Similarity
Matches 13; Conserv
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Direct Submission

AL Submitted (12-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Bairren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N. Bastlen, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barra, N. Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chango, J., Conopel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gorde, S., Goyette, M., Gadam, L., Grand-Pierre, N., Gardyna, S., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Macton, L., Hulme, W., Iliev, I., Johnson, R., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., McKernan, K., Maldrim, J., Menuers, L., Manga, V., Murphy, T., Naylor, J., Mouyen, C., Nicol, R., Norbu, C., Necerson, K., Phunkhang, P., Pierre, N., Pollerar, V., Poller, V., Poller, R., Stene, C., Roger, P., Spencer, B., Stanger, T., Pleodore, J., Oconnor, T., Obonnell, P., Oliver, J., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Stene, C., Roger, P., Spencer, B., Stanger-Thoman, N., Stone, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vow, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Blirect Submission

AL Submitted (25-MAR-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Calangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Brown, A., Castle, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitziugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., Fitziugh, W., Forrest, C., Funke, R., Gage, D., Horton, J., Galagan, J., Gardyga, S., Grant, G., Kann, L., Karatas, A., Horton, L., Howland, J.C., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Horton, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Say, A., Santos, R., Severy, P., Peterson, K., Pollara, V., Riley, R., Subamanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                          128957 GAAAAATACATCCTGATGACTTCAGACAGAAGGAAGAAGGAGGAGGACAAGTGATTGGTTG 128898
129077 AATAGGAAGGTGAGAACATGGTATTCCCTCGGACCTATAATTTAAAGGATAAGTTGAAAC 129018
                                                                                           129017 ICTICGGICCAATAAGAGGAAGGACGIGTTTCATTCAGAGGCTCAGAGGTGAGGCTCA 128958
                                                                                                                                                                                                                                                                                                                                                                                                                            AC012294 222121 bp DNA linear ROD 27-MAR-2002
Mus musculus chromosome 11, clone RP23-328G11, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 222121)
Bliren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-328G11
                                                    TCTTCAGTCCAATGA----GGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCA
                                                                                                                                                   294 G-GAAAIGTAACTTATAGATTTTATACATACACAGAAATACGGACTAGTGAGAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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.larity 55.5%; Pred. No. 3.8e-05;
Conservative 0; Mismatches 151; Indels 11; Gaps
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of 2235
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of 4176
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10.1%; Score 60.4; DB 10; Length 222121;
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.26722. .26248
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.26241. .26342
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.7rpt family="L3_MM"
.7rpt family="L3_MM"
.26655. .26722
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Complement(1910. .19022)
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Birren, 320 Charles Street, Cambridge, MA 02141, USA

Anderson, S., Banda, N., Batien, V., Bloom, T., Boguslavky, L.,
Boukhgalter, B., Brown, A., Calmarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Coheel, Y., Colangelo, M., Collins, S., Collymore, A.,
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Viel, R., Vo, A., Wilson, B., Whitehead Institute/MIT Center for Genome
Strauss, N., Subramanian, A., Taalamas, J., Ye, W.J., Young, G.,
Direct Submission

Direct Submission

Londer S., 2002 this sequence version replaced gi:19683729.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp:genome.washington.edu/RM/RepeatMasker:html
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Center: Whitehead Institute/ MIT Center for Genome Research
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Web site: http://www-seq.wi.mit.edu
Contact: sequence ubmissions@genome.wi.mit.edu
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complement(1. .315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403. ..560
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                   REFERENCE
AUTHORS
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AL713839.1 GT:19682818
S6M1-SP6; DIBHm140; DIIMit354; DIIMit66; DDK syndrome; Mdeg; Ovum
mutant; Scya2,11,7,8,12,1.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Submitted (20-MAR-2002) Genoscope - Centre National de Sequencage :
Submitted (20-MAR-2002) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9155 gaaaaatracircigardacricagacadacadadaaaadaadadadadadadadadarda 9096
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Cohen-Tannoudji M., Vandozmael-Pournin S., LeBras S., Coumailleau Cohen-Tannoudji M., Vandozmael-Pournin S., LeBras S., Coumailleau F., Babinet C., Baldacci, P.
Unite de Biologie du Developpement, CNRS URA 1960, Institut Pasteur, 25 rue du Dr Roux, 75724 Paris cedex 15, France.
Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9335 GAĠCTGĊATGTATAİCAAGAGATGGGGATTİTTCAAGAĞGAAĞCİCAAİACAĞGĞTİTĞĞ 9276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9275 aataggaaggtgagakcatggtattccccggaccrataatttaaaggataagttgaaac 9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus chromosome 11 region in the Om locus area (D11Mit37-Scya6) clone 149H13 of library Caltech CITB-BAC from AL713839
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                                                                                                                                                                                                                                                                                                                                                                         9452 TAGGAAAAAACACAAAAGCATTAAGGAAAACTGGTAGGTGGGGGAAATTATCCAAAAA
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                              Length 223726;
                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                   Score 60.4; DB 10; Length
Pred. No. 3.5e-05;
0; Mismatches 151; Indel8
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                                         /organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                   /chromosome="11"
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/clone_lib="RPCI-23"
location/Qualifiers
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55.5%;
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Direct Submission

Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (04-APR-2002) Wellcome requests: clonerequestgesnger.ac.uk Clone requests: clonerequestgesnger.ac.uk On Nov 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version replaced gi:17065774.

On Mov 30, 2001 this sequence version replaced gi:17065774.

On Mov 30, 2001 this sequence version replaced sa variations where differences are found these are annotated as variations where the the corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequence with an alternate regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = chemistry or covered by high quality data (i.e., phred quality) = as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the one plasmid subclone or more than one Mi3 subclone; and the abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                    100157 GAĞCTGCATATATCAAGAGATGGGGATTİTTCAAGAĞGAAĞCİCAATACAĞĞĞTİTĞĞ 100098
                                                                                                                                                                                                                                                                                                                                                                                                                                   100097 AATAGGAAGTGAAGAACATGGTATTCCCTCGGACCTATAATTTAAAGGATAAGTTGAAAC 100038
                                                                                                                                                                                                                                      100214 TAGAAATGAAAATGGTGTGTACATTAAACGGGGAAAGAGGGAAAGCATCCG---ATG 100158
                                                                                                                                        100274 TAGGAAAAAAACACAAAAAGCATTAAGGAAAACTGGTAGGTGGGGAAATTATCCAAAAA 1002115
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223726 bp DNA linear ROD 05-APR-2002
Mouse DNA sequence from clone RP23-350G1 on chromosome 11, complete
sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                 Gaps
                                                    11;
                            55.5%; Pred. No. 3.5e-05;
tive 0; Mismatches 151; Indels
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Mus musculus
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                                                 Best Local Similarity 55.5
Matches 202; Conservative
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                                            Local Similarity
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DOE Joint Genome Institute.

Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center.

Center: Joint Genome Institute
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                  Indels 11; Gaps
                                                                                                                 Length 240425;
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Consensus quality: 143665 bases at least Q40
Consensus quality: 160562 bases at least Q30
Consensus quality: 164105 bases at least Q20
                                                                                                             Score 60.4; DB 10;
Pred. No. 3.5e-05;
0; Mismatches 151;
/db_xref="taxon:10090"
/chromosome="11"
/clone="149H13"
/clone_lib="Caltech CITB-BAC"
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Center clone name: RPCI-23_92G22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.jgi.doe.gov
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ACO73824
ACO73824.1 GI:8810441
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house moüse)
Mus musculus (house moüse)
Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Rodentia; Sch
DoB Joint Genome Institute.
                                                                                                             Query Match
Best Local Similarity 55.5%;
Matches 202; Conservative
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                                                                          ORIGIN
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8

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Estimated insert size: 194000; pulse field gel estimation
Estimated insert size: 176244; sum-of-contigs estimation
Quality coverage: 6.92 in Q20 bases; pulse field gel estimation
Quality coverage: 7.62 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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of 1406 bp in length
unknown length
of 1119 bp in length
unknown length
of 1339 bp in length
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Local Similarity 54.8%; Pred. No. 0.00055;
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contig of 9267 bp in length
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/mol_type="texon:10090"
/clone="RP23-92G22"
/clone_lib="RPCI mouse BAC library 23"
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                                                     AL SUDMILTEATOR.

Submitted (108-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 14, 2002 this sequence version replaced gi:21737094.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', Mithin each contig-scaffold', Mithin each contig-scaffold', Mithin each contig-scaffold', Mithin each contig-scaffold', Mithin each contig-scaffold's and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be preserved.

* The finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 0.990329
Consensus quality: 233717 bases at least Q40
Consensus quality: 236719 bases at least Q30
Consensus quality: 236622 bases at least Q20
Estimated insert size: 252037; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                Genome Sequencing Consortium.
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/note="wgs_contig"
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/note="wgs_contig"
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Matches 111; Conservative
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Marny, D. Marte., Marker, M. Lee., Abramazon, S., Adams, C., Alder, J., Alaborooks, S., And., A., Anguiano, D., Allaen, C., Allaen, H., Alsbrocks, S., And., A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Barteleed, M., Benahmed, F., Balddrin, D., Bandaranaike, D., Barter, M., Barstead, M., Benahmed, F., Balddrin, D., Bandaranaike, D., Barter, M., Cae, A., D'Soura, J., Carter, K., Balddrin, D., Bandaranaike, D., Barter, M., Cree, A., D'Soura, J., Carderia, V., Carter, K., Baldrin, D., Bandaranaike, D., Barterla, M., Cree, A., D'Soura, J., Carderia, C., Carver, M., Carter, M., Cree, A., D'Soura, J., Carderia, C., Corkell, R., Cox, C., Coyle, M., Cree, A., D'Soura, J., Doulado, O., Denson, S., Derson, C., Coyle, M., Cree, A., D'Soura, J., Doulada, Corte, B., Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Derson, C., Duttin, K., Dutal, B., T., Fan, G., Perport, M., Dugan, Rockon, S., Derson, C., Ding, Y., Chall, C., Dray, Carroll, L., Derson, C., Dever, C., Carroll, L., Derson, C., Corte, M., Carte, M., Carte, M., Carte, M., Gerer, M., Gerer, K., Ganta, R., Garte, M., Garter, M., Gavara, M., Gherson, S., Derson, C., Manli, C., Hamilton, C., Hamilton, K., Harvey, Y., Harvak, P., Hawse, A., Henderson, M., Hernandez, B., Haldun, S., Haldun, S., Haldun, S., Haldun, S., Haldun, S., Haldun, S., Haldun, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Manden, M., Martin, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mortis, R., Mo
                                                                                   119950 AGTTTATACAATTTGTCAGCCAGACAGGAAAAAGGATACACCGTTCCCAAGGTCAACACT 119891
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Rattus norvegicus clone CH230-33A7, WORKING DRAFT SEQUENCE, 4
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
382 GGCCTAAATATGGAGCCAAAGGGCAGCAATGAAGAATGAGCCATGCAGGGTGAAATGCT
                                                                                                                                                                                                                                                         119890 ccarctracacceracarcaacaaccricraaarrca 119854
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Direct Submission

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department Submitted (15-NOV-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Daylor Plaza, Houston, TX 77030, USA

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using described in the facture table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                   2. (bases 1 to 239429)
Morley, Kr.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 239429)
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A. Direct Submission Unpublished
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3408: gap of unknown length
157094: contig of 153686 bp in length
157194: gap of unknown length
237986: contig of 80792 bp in length
238086: gap of unknown length
239429: contig of 1343 bp in length.
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clone_end:T7"
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/db_xref="taxon:10116"
/clone="CH230-33A7"
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/note="clone_boundary
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172706 GCCGAÀAGAACATGGAGGTGGTTAAGGTTCCTCTCTGCACATTGCAGGTTATGAAT 172647
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                                                                                                                                                                                                                                                                                                                         91 GGGAGAAAACCAATGAACCAGATGCGAATTCGGGCCCACACCAATGTCAAGGGATGACAA 150
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                                                                                                                                                                                             Gaps
                                                                                                                                         Query Match

7.4%; Score 44.6; DB 2; Length 239429;
Best Local Similarity 53.1%; Pred. No. 0.38;
Matches 95; Conservative 0; Mismatches 84; Indels 0;
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                                   end sequence:BH351359"
3409. 5768
/note="wgs_contig"
clone_end:T7
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2003ds:\*

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geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\*

geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\*

geneseqn2004as:\* geneseqn2004bs:\*

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SUMMARIES		ID	ADEL 2020	AD003803	ACN44342	ADA71938	ADN30166	ACN44062	ADR64667	AAD28378	ABK39967	ADA02738	ADB72476	ADC85218	ADM74333	ADA71938	ADR07244	AAS46669	ACN44934 3	ACN44934_2	ABK83568 _	ABL45715
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		Score	009	009	41.2	40.8	39.4	39.4	38.8	38.8	38.4	38.2	38.2	38.2	38.2	37.4	37	37	37	37	36.6	36.4
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## ALIGNMENTS

RESULT 1

ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:1. Poustka A; Delius H, Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. ADH13938 standard; DNA; 600 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. EP1170372-A1. Homo sapiens 09-JAN-2002. ADH13938; ADH13938 

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.

Disclosure; SEQ ID NO 1; 30pp; English.

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiatreriosoclarotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

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16-OCT-2003;
              30-OCT-2002;
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   the treatment
                                                                                                                                                                                                                                                                                                                     AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA
                                                                                                                                                                                                                      TCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG
                                                                                                                                                                                                                                TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG
                                                                                                                                                                                                                                                                   GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGGAGGCAGCAATGAAGAATG
                                                                                                                                                                                                                                                                                                      GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGGCAGCAATGAAGAATG
                                                                                                                                                                                                                                                                                                                                TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT
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                                                                                                                                                                                                  TAGAAATGGTGATGATGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATT
                                                                                                                                  AATGTTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
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pharmaceutical composition of the invention is useful for the of diseases associated with dysregulation of MCP-1 expression, atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                          Length 600;
                                         Sequence 600 BP; 213 A; 101 C; 150 G; 136 T; 0 U; 0 Other;
                                                                         0; Indels
                                                         ; Score 600; DB 6; I
; Pred. No. 2.3e-173;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Cc12 gene and enhancer region
                                                                                                                                                                                                                                                                                                                                                                                                                                                ВЪ
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                                                            100.0%;
ilarity 100.0%;
Conservative 0;
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                                                              Query Match
Best Local Similarity
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                                                                      Best Local Simi
Matches 600;
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10279 TAACTTATAGATTTTATACATACACAGAGAATACGGACTAGTGAGAAGCTATTGCCATG 10338
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to addinistering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or inpofuscin mouse eye for development or regression of drusen and/ or lipofuscin membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                        Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient Knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9979 TAGGAAAATTATAGGATCATTAAGAAAGGAAGAGGAAGAGGAGGAGGAAGAGAAATTATAGGAAGATACCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10039 TAGAAATGGTGATGATGTGTACATCAAGGAGAGAAAAACCAATGAACCAGATGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGTTAGGGTGAAAAGTTACTCAACTCTGTAGGTTAAAAAGGAAACGTTGAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGTCCAATGAGGAGGGATGTGCCATGTTAGAGATTCAGAGATAAGTTTCAGGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 11793;
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100.0%; Pred. No. 9.1e-173;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 4; 64pp; English.
                                                                                                          RES FOUND
                                                      2002US-0422096P.
2003WO-US032933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          accumulation in eye.
                                                                                                                                                                                                                     WPI; 2004-400512/37.
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10158

10218

Plant; bacterial infection; fungal infection; viral infection; rice;

(first entry)

20-NOV-2003

Rice gene, SEQ ID 5263

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                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for secreening drug candidates; (ii) for secreening of bioactive agent capable of biding to Carcinoma secreening (AP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (ix) for the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent.
10519 GTTTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 10578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCACAAGGAACAGCAGGTACAAAGGCTCGGAGGTCGAATGAACTTAATGTGTTCACA 9468
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                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78268 BP; 20402 A; 18203 C; 18818 G; 20845 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 41.2; DB 11; Length 78268; 62.7%; Pred. No. 0.55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 AAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCGGGCCC 127
                                                                                                                                                                    Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence.
                                                                                                                                             Human genomic sequence hCG17932.
                                                                       ACN44342 standard; DNA; 78268
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 742; Opp;
                                                                                                                                                                                                                                                                  28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                           01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA71938 standard; DNA; 2000
                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-328604/31.
                                                                                                                                                                                                                  WO2003073826-A2
                                                                                                                     18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                     comprises a
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                                                                                               ACN44342;
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ID ADA7193
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AC ADA7193
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                                                  RESULT 3
                                                              ACN44342
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Hou Y; T, Zou

Goff SA, Hor Z, Zhu T,

Glazebrook J, G Whitham S, Xie

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Cooper 1 S, Tao

Katagiri F, Quan S,

Chen W,

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Chang

WPI; 2003-175290/17

gene expression

(SYGN ) SYNGENTA PARTICIPATIONS

22-JUN-2001; 2001WO-IB001105

WO2003000898-A1

03-JAN-2003

Oryza sativa

gene; ds.

Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant

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                                                                    The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is bacterial, fungal or viral infection. The present sequence to a plant to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TAGAAATGGTGATGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 MAKWYWATGWATWMWRYTWYTYCYAMTCAKCKYKMAMTKWWTTWACAWRATSWRWRAM 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             806 GINEWKRYKONKRAYWWRWWRCWKAGWARWMKSRYRWKWKKYATRYYWKWMAMTWWWSWRRW 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAAAACCCTGTGACTTCAGA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 ISCMWWKYWRIWSCWYIMWWGAMRYAYYAMRRRRWTYKWSWRRMYWIMIKWAWIWMICMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 40.8; DB 8; Length 2000; 10.6%; Pred. No. 0.14; ive 228; Mismatches 255; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative 228; Mismatches
Claim 27; SEQ ID NO 5263; 899pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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96760 AattaCACAAAATATTTCACCTCTGAAAAAATACAAAGAAACGGAACTTAACTA 96701
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une present invention integrate to move, where the series are useful for: (i) for screening drug darking darkes; (ii) for screening of bloactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bloactive agent capable of modulating the activity of CAP; (iv) for diagnosing evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating; carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma as propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number: In addition, the determining Carcinoma Associated (CA) gene copy number: In addition, the carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This parent is an equivalent to basic patent upsated using the capable patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 144035 BP; 43371 A; 28888 C; 27578 G; 44198 T; 0 U; 0 Other;
                                                                                                                 407 AGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.4; DB 11; Length 144035;
Pred. No. 2.6;
0; Mismatches 91; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 322; Opp; English.
                                                                                                                                                                                                                                                                                                                                   ACN44062 standard; DNA; 144035 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genomic sequence hCG38705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                              88077 CATAT 88073
                                                                                                                                                                                CCTGT 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Best Local S
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                                                                                                                                                                                                                                                                                                                       ACN44062/c
                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a new compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding hepatocyte growth factor receptor, where the compound specifically hybridises with the nucleic acid molecule encoding hepatocyte growth factor receptor comprising a sequence of 4586 bp (SEQ ID NO: 4) and inhibits the expression of hepatocyte growth factor receptor in cells inhibiting the expression of hepatocyte growth factor receptor in cells or tissues; screening for a modulator of hepatocyte growth factor in cells receptor; a diagnostic method for identifying a disease state, a kit or assay device comprising the compound; and treating an animal having a disease or condition associated with hepatocyte growth factor receptor. The compound and methods are useful in diagnosing and treating having a hyperproliferative disorder. This sequence represents a human, hepatocyte provite accounts.
                                                                                                                                                                                          541 GITICCCTCCATTACTATACCCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 600
                                                                                                                                                                                                                    CWYYYYGMYMKCSYMWRYGYCKACKACCYAMCWKAAYSGMMYWYRKYSKWMRMSTKYMW 447
                                                                                                                             566 MRKRKYMRYMKWKCTWRRCMCYRWGYTWYTTSRSRMMYTGRYKARYTSKRRYMWYKYRKY 507
                               626 MSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRMSGMSRNYMRWWKK 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88257 katitackcakakitatatittcaccicickakakakitackakkakakitakacta
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                                                                                                   481 TAIGAAAACCICAICTICAACCCACAITITAAGGGGGGCAGCIICCCIGAAACCAGAAIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compound targeted to a nucleic acid molecule encoding hepatocyte growth factor receptor, useful in diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.4; DB 12; Length 126974;
Pred. No. 2.5;
0; Mismatches 91; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; hepatocyte growth factor receptor; human; ds. hyperproliferative disorder; antisense technology; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth factor receptor associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatocyte growth factor receptor associated DNA
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                                                                                                                                                                                                                                                                                                                                                                ADN30166 standard; DNA; 126974
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50.8%;
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hyperproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-399741/37.
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Homo sapiens

27-MAY-2004

Dean NM,

12-AUG-2004

ADN30166;

ADN30166/c

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Query Match Best Local Si Matches 94;

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WO200202809-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC sequences mentioned in the specification and producing a plant having an improved property.

CC comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoterty, and growing the transformed plant. The polypetide associated with the property, and growing the transformed plant. The polypetide is cuseful for improving plant cold tolerance manipulating growth rate in plant tolerance, providing increased resistance to plant disease, coroughing plant cold tolerance manipulating growth rate in plant tolerance, improving plant tolerance to plant disease, coroughing increased resistance to herbicides, increasing plant heat tolerance, improving plant tolerance to herbicides, increasing colducing galactomannan (or lignin or plant growth regulators) improving plant tolerance concern; improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants; improving pield by modification of photosynthesis, modifying seed oil or protein yield by modification of content, improving yield by modification of carbohydrate, introgen corpus, improving yield by modification of plant growth and development under at least one stress condition. The plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA
                                   407 AGCAATGAAGAATGAGCCATGCAGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAAGA 466
                                                                                                                                                                                                                                                                                                         Cotton, 88; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5448; 14pp; English.
                                                                                                                                                                                                                                                                             Cotton cDNA sequence, SEQ ID 5448.
                                                                                                                                                                                 ADR64667 standard; cDNA; 1768 BP
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12-DEC-2001; 2001US-00021323
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                                                                                                    96580 CATAT 96576
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                                                                       CCTGT 471
                                                                                                                                                                                                                                                                                                                                                                                         resistance
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1402 ATAAGAAAGGAAACATAAGAGAAGACGAAATAAAAAATAGATGGTGGAAGTGATAAAA 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1223 ACAAAGTATACAATACATATAAAAAAAAGTCACAAGGAAAAATAAAAGTACTAGAAACA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 ACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAACTTA 307
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constructs, in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence is a Cotton plant cDNA of the invention. NOTE: The sequence data for thi patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence is commat directly from USPTO at sequence. The sequence were available, the remaining 52213 polymucleotides and all 58798 protein sequences were not present.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.8; DB 13; Length 1768; Pred. No. 0.53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 162; Indels
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Best Local Similarity 47.4%;
Matches 147; Conservative
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01-SEP-2000; 2000DE-01043826.
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Homo sapiens.
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(SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1182 ĠGTÄGTŤTTÄĠTGGÄAAATŤGTRGÄŢĞTÄÄĞGĠTAĞÄTĞTÄÄGGÄĞTTÄÄATĞŤTTÄĞĞ 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1242 İTTALTATGATAAĞİTTCGAAİTAGAATATATTTTAATTTGİĞİTTATTAGİAAAĞGG 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                               The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligomuclectides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful tor the diagnosis or therapy of behavioural disorders, neurological for the diagnosis or therapy of behavioural disorders, neurological syndrome, schizophrenia, psychiatric and neurological disorders, smoking, syndrome, schizophrenia, personality traits, compulsive gambling, human drug abuse, alcoholism, personality traits, compulsive gambling, human schizoaffective patients, and suicidal behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation schizophrenia. The nucleicides and/or single nucleotide polymorphisms (SUDS) when recent someoners in human consists of all CPG dinucleotides and/or single nucleotide polymorphisms (SUDS) when recent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GGAAGGTTGAGTCAAGGGGATTTGAATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 TTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGAT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP1AA; CYP11B1; CYP3A3; DPYD; BFHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                      state of all CpG dinucleotides and/or single nucleotide polymorphism:
(SNPs). The present sequence is human chemically treated genomic DNA
    Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of esgment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7340 BP; 1725 A; 249 C; 1982 G; 3384 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 7340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chemically pretreated gene sequence #24 strand 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 38.8; DB
54.1%; Pred. No. 1;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1302 AAAGAAAGAAATGAATAAAGTTAA 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGAGATAAGTTTCAGGAAATGTAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                           Claim 1; Page 94-98; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2001; 2001WO-EP007470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK39967 standard; DNA; 8943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-154757/20.
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The invention relates to a nucleic acid comprising a sequence at least 18 conserved by asset in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the associated with pharmacogenomics according to one of the sequences of the genes ALDHG (NM 000693), CYPIJA (NM 000776, IM 000697), CYPJA3 (SM 000776, IM 000693), CYPIJA (NM 0003160), MRP (NM 0004996, IM 019900, IM 019901, NM 019900, NM 019900, NM 019901, NM 019902, NM 019862, NM 019808, NM 019909) and CC (NM 000776, IM 019901, NM 019902, NM 019862, NM 019808, NM 019909) and CC their complements. The chemical pretreatment is bisulphite sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. CC treatment to convert cytosines (but not methyl-cytosines) into uracils. CC treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligomer or a passociated with complements, arranged in an array for identical to a chemically pretreated DNA of genes associated with the methylation state (Cp) and/or analysing diseases associated with the methylation state (Cp) and/or analysing diseases associated with the methylation state (Cp) and/or analysing diseases associated with the methylation state (Cp) and/or analysing diseases associated with the methylation state (Cp) and/or and their complements is useful for diagnosis and therapy of solid and cancer. The present sequence date for this patent did and their complement. Note: The sequence date for this patent did electronic format directly from WIPO at celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3258 Aritnggirnágraagriágáraraaaitárrárritarrádárrártíritáarráátárr 3317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3198 tattigargadadatritatritritritritisaandadadaanatsaana 3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AGTCCAATGAGGAGGAATGTGTGTTTAGAGATTCAGAGATAAAGTTTCAGGAAATGTA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IGITAGGTGAAAGTTACTACTCAACTCTGTAGGTAAAAGGAAACGTTGAAAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8943 BP; 2415 A; 42 C; 1943 G; 4543 T; 0 U; 0 Other;
pharmacogenomics and for therapy of diseases e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CCND2 carcinoma associated gene, SEQ ID NO:1256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3318 GTİTTİAAİTİTİTİTTİTATTAAAGATGAATGAGGGGAG 3357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 ACTTATAGATTTTATACATACAGAGAAATACGGACTAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                         Claim 1; SEQ ID NO 48; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 52.5%;
Matches 84; Conservative
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The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence salected from any of the 600 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polymptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                  recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 38.2; DB 10; Length 52302; 69.3%; Pred. No. 3.8; cive 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                 cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 304; 2304pp; English.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Conservative
                                                     (SAGR-) SAGRES DISCOVERY
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Best Local Similarity
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                                                                                                           Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC85218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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     8X4X1X8X14X8X2CCCCCX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protonnocegenes. The CA nucleic acid sequences can be used to diagnose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as present sequence represents a specifically claimed human CA nucleic acids present sequence are also useful as present sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 AGGAGAAGGAAGAGTGGGAGCAAATACCTGGAGGTAGAAATGGTGATGTGTACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
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                                                                                                                            New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 52302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            Claim 1; SEQ ID NO 1256; 245pp; English.
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; 2001US-00004113.
; 2001US-00052482.
; 2001US-00997722.
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                                                                      WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CCND2 gene
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23-OCT-2001;
08-NOV-2001;
30-NOV-2001;
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50950 AGCAGAAGGAACAGAGAATGCAAAAGATCCGGAGGTAGGAATGAGCATGACGTGGTCTACG 51009
                                                                                                                                                                                                                                                                                                          Cytostatic, gene therapy, vaccine, cancer, carcinoma-associated gene, CA; secreted, transmembrane, intracellular, ds.
27 AGGAGAAGGAAGGGAGCGAAATACCTGGAGGTAGAAATGGTGATGTGTGTACATCA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant nucleic acid comprising a
nucleotide sequence selected from any of the fully defined carcinoma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4; 983pp; English.
                                                                                                                                                                             ADC85218 standard; DNA; 52302 BP
                                                                                              51010 AACAGAGAGAGGCCC 51024
                                                                                                                                                                                                                                                                           Human Cond2 genomic sequence.
                                                              87 AGCAGGGAGAAAACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2002; 2002WO-US038582
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                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Engelhard EK;
                                                                                                                                                                               CCXXX4111X8X1X8X1X4X6X8X8X8X8X6X1X8X1
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Oryza sativa.
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Katagiri F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA71938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to new recombinant nucleic acids. The invention calso relates to a host cell comprising a recombinant nucleic acid or also relates to a host cell comprising a recombinant nucleic acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma drug, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of for inhibiting carcinoma, an enchod of capanosing carcinomas, a method of method of evaluating the effect of a candidate contralising the effect of a CAP, and method of evaluating the effect of a candidate propensity to carcinoma. A method of evaluating the effect of a candidate contransmant of carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering alterations in the
                                                                                                                                                                                ö
                                                                                                                                                                  86
associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                27 AGGAGAAGGAAGAAGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATÇA
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                 Seguence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                             DB 10; Length 52302;
                                                                                                                                         ö
                                                                                                                                           Indels
                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                  Human carcinoma associated (CA) nucleic acid #1.
                                                                                                               6.4%; Score 38.2; DB
69.3%; Pred. No. 3.8;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4; 29pp; English.
                                                                                                                                                                                                                                                                                                                      ADM74333 standard; DNA; 52302 BP.
                                                                                                                                                                                                                                                      51010 AACAGAGAGAGCCC 51024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-2000; 2000US-00747377.
02-MAR-2001; 2001US-00798586.
                                                                                                                                                                                                                             87 AGCAGGGAGAAAACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-328562/30.
                                                                                                           Query Match
Best Local Similarity
....heg 52; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphoma.
                                                                                                                                                                                                                                                                                                                                                       ADM74333;
                                                                                                                                                                                                                                                                                                 RESULT 13
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expression or activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of method of diagnosing carcinoma comparing the expression of the gene first individual and comparing the expression of the gene from type of a first individual and comparing the expression of the gene from that the first individual, where a difference in the expression indicates unaffected individual, where a difference in the expression indicates that the first individual has carcinoma. A method of inhibiting the carcinomas comprises binding an inhibitor to the CAP. Treating carcinomas comprises administering to a patient a inhibitor of CAP.

Correspond to the CAP comprises contacting an agent specific Neutralising the effect of a CAP comprises contacting an agent specific CAP the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acid is to nucleic acid. The nucleic acid. The nucleic acid. The nucleic acid in a composition for diagnosing or treating carcinoma e.g., proper in a composition for diagnosing or treating carcinoma e.g., corrected to the protein capt and not form that specification but was contained in electronic format directly from USPTO at contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50950 Accadadodakcadadanaccadadanccoddadograddadandadacandaconcondos 51009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method (M1) for identifying genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AGGAGAAGGAAGAGGAAATACCTGGAGGTAGAAATGGTGATGATGTGTGTACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; bacterial infection; fungal infection; viral infection; rice;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 52302;
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Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
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Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 38.2; DE
59.3%; Pred. No. 3.8;
ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA71938 standard; DNA; 2000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51010 AACAGAGAGAGCCC 51024
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AGCAGGGAGAAACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity o...
Best Local Similarity o...
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice gene, SEQ ID 5263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Cor
F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-175290/17.
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involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                  62 AGAAATGGTGATGATGTACATCAAGCAGGAGAAAACCAAATGAACCAGATGCGAATTC 121
                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                 327 KKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYYWRWRWRWRWTRRRRWAKKSSRTSRRK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 KRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRAWKWGCKGCMTCRMKSYGMMRWKS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 KRSSAKRYAMMGGMISGSRMSRWKSYICYWRKWGSMKSICIWMYYMSKYIYAKYGSYWRY 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 ATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGTG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full length human cDNA useful for treating neurological disease Seq 750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; 88; human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; barkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                           267 RKMRWSRSYGWYSWSYKMWCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRMAMMY
                                                                                                                                                                                                                                                                                                                                                                          ATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTCCAATGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 KMMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMCKRSKMSAWSKSMRSSRKCRKCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 GCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGAT
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                        Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                             DB 8; Length 2000;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                       Best Local Similarity 8.4%; Pred. No. 1.5;
Matches 43; Conservative 237; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 TITCCCTCCATTACTATACCCCCATCCCA 570
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                                                                                                                                                                                                                         6.2%;
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to constitute obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as cartibodises, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these to and modulate expression of the CDNA molecules. They are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or mortor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquilliser activities. This sequence is not always in the sequence listing of the specification but can be obtained on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800 TATTAAGAAATGATAGGAACATTGACACTAATGTGGAGGAATTTGCCAAATATTTTATTT 1859
                                                                                                                                                                                                                                                                                                        New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 TAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATT
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                                                                                                                                                                                        Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2646 BP; 845 A; 450 C; 495 G; 856 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD-ROM from the European Patent Office, Vienna Sub-office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                      Nishikawa T, Isono Y,
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 750; 2686pp; English.
                                                                                                                                                  (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                          14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
                                                      12-FEB-2004; 2004EP-00003145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%;
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                                                                                                                                                                                      Yamamoto J,
                                                                                                                                                                                                                                                WPI; 2004-583265/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                      Isogai T, Ya
Wakamatsu A,
                18-AUG-2004.
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LD4038/1 514 bp DNA linear GSS 27-SEP-2003 tigr-gss dog-17000363267544 Dog Library Canis familiaris genomic, genomic survey sequence.
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Contact: Kirkness BF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-638-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis. I tosel 1 to 51. Kirkness E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a Determination with the Berkeley Drosophila Genome Project (BDGP). Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila The BDGP is constructed a physical map of the DGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by the BDGP brosophila NY. The library is named RPCI-98 and was constructed by partial NY. The library is named RPCI-98 and was constructed by partial BC-Cancer Instruction of Drosophila DNA provided by the BDGP from the EGORI digestion of Drosophila DNA provided by the BDGP is and how to order individual BAC clones, the entire library, or and how to order individual BAC clones, the entire library, or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TBT3 end of BAC # BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit AL060767
                                                                                                                                                                                                                                                                                                                                                                                           298 ATGTAACTTATAGATTTTATACATACAGAGAAATACGGACTAGTGAGAAGCTATTGCC 357
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Eudopterygota; Diptera; Brachycera; Muscomorpha;
Behydroidea; Drosophilidae; Drosophila.
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PW B192 by www.genoscope.cns.fr)

Collaboration of this BAC-end sequence was carried out as part of a petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

Collaboration with the Berkeley Drosophila Genome Project (BDGP).

Collaboration with the Berkeley Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Drosophila Dros
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR01M22 of RPCI-98 library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bokaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Neophera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Dphydroida; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                     62 AGAAATGGTGATGATGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTC
                                                                                                                                                                                                                                                                                                                 182 ATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT
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524 RRARRARRRRRRGGARRRGGRRRAAGARAARA 480
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4.1e-07:
       ch
1 Similarity 18.5%; Pred. No. 4.1e-07;
86; Conservative 173; Mismatches 206;
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqrefégenoscope.cns.fr - Web : www genoscope.cns.fr) effective is sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster ARC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCCAA 249
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                                                                                                                                                                                                                                                                                                                      70 TGATGATGTGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTCGGGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 ACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                        Length 1101;
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
                                                                                                                                                                                                   8.3%; Score 49.6; DB 9;
ilarity 19.5%; Pred. No. 0.015;
Conservative 144; Mismatches 133;
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AL063921
                                                                                      /clone lib="DrosBAC"
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/note="end : T7"
                                                                   /clone="BACN03K20"
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                                                                                                                                                                                                                                                                                                                                                                                                          65 AATGGTGATGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCGGG 124
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                                                                                                                                                                                                                           Length 1101;
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                                                melanogaster"
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Drosophila melanogaster
                           1. .110]
/ organism="Drosophila mel/organism="Drosophila mel/mol type="genomic DNA"
/ db_xref="taxon:727"
/ clone="backolus2"
/ clone=lib="RPOT-98"
/ note="end : TET3"
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Location/Qualifiers
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AG287979 171 bp DNA linear GSS 02-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-061N22.TJ, genomic survey
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2. On bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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12 (bases 1 to 771)
13 (bases 1 to 772)
14 attori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Phy
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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BAC end Sequences of Library MSMg01
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| G18 GARRGERRARRARRAGARRAGRRAGRRAGARA 574
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Best Local Similarity 22.5%; Pred. No. 0.045;
Matches 91; Conservative 121; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                           melanogaster"
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/organism="Drosophila mel"
/organism="Drosophila mel"
/ol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROGIG"
/clone=lakCROGIG"
/clone=lib="RPGI-98"
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DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRO9CIG of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                             303 ACTIAIAGAITITAIACAIACACAGAGAAAIACGGACIAGIGAGAAGCIAITGCCAIGGI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAGCAAGAAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAGA 422
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
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ilarity 12.9%; Pred. No. 0.019;
Conservative 233; Mismatches 163; Indels 3
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                                                                                                          /organism="Drosophila mel.
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACROSK10"
/clone="tb="RPCI-98"
/note="end : TET3"
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AL108811.1 GI:5629115
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr.
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and mannoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)

Tel:81-45-503-911, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba institude, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

KOyadai, Tsukuba, 305-6074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="mixture of kidney and spleen" clone_1ib="msmg01 mouse male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus molossinus"
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                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-061N22.TJ"
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AL065414
AL065414.1 GI:4938827
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EcoRI
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R.Site 2
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 ATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT 241
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NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Esogenic strain used for the BDGP in the BDGP and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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| forganism="Drosophila melanogaster" |
|/mol type="qenomic DNA" |
|/db xref="taxon:7227" |
|/clone="BARGROIJG" |
|/clone="lab="RPCI-98" |
|/note="end : TET3" |
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ORIGIN

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1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC:
BACK29M06 of RPCI-98 library from Drosophila melanogaster (fruit RIY), genomic survey sequence.
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Submitted (02-UU1-1999) Genoscope - Centre National de Sequencage :
Submitted (02-UU1-1999) Genoscope - FRANCE (E-mail : segref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boxpera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGAAAATTATAGGATCATTAAGAAAGGAGAAGGAAGAAGAGTGGGAAGAAATACCTGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                            // Organism="Sorghum propinguum"
/organism="Sorghum propinguum"
/orlow="Sorghum propinguum"
/db xref="teaxon:132711"
/clone="SP_Ba0082111"
/clone=lbb="SP_Ba"
/note="Voctor: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Paterson lab BAC library (HindIII)"
                                                                                                                                                                                                                                                                                                                                                         Length 1181;
                                                                                                                                                                                                                                                                                                                                                           Query Match
Pest Local Similarity 44.4%; Pred. No. 0.43;
Matches 185; Conservative 0; Mismatches 231;
                                                                                                                         S
                                                   PCR PRIMERS
FORWARD: atc agc ggc cgc gat cc
BACKWARD: gta aaa cga cgg cca gtg
Plate: 0082 row: I column: 11
Seq primer: atc agc ggc cgc gat cc
Class: BAC ends.
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                           Location/Qualifiers
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
I dade; Panicoidaea; Andropogoneae; Sorghum.
(bases 1 to 1181)
Wing,R., Yu,Y., Kim,H.R., Collura,K., Pries,G., Currie,J.,
Sequencing, C. and Hatfield,J.
Sequencing of Sorghum BAC ends.
http://genome.arizona.edu/stc/sorghum
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 RRKRDARKTARDGGRRARTRRRAWAAGGKRARAGARRARAARRAADDRDWDAWAAAAA 837
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                                                                                                                                                                                                                                                                                                      5 AAAATTATAGGATCATTAAGAAAGGAGAAGAAGAAGAGGAGCAAATACCTGGAGGTAGA
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS SP Ba0082111.f SP Ba Sorghum propinguum genomic clone SP Ba0082111.f s', genomic survey sequence.
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7.5%; Score 44.8; DB 9; I
Best Local Similarity 26.3%; Pred. No. 0.33;
Matches 121; Conservative 129; Mismatches 209;
                                                                                  /mol type="genomic DNA"
/db_xref="taxon:727"
/clone="abANN 3D10"
/clone lib="brosBAC"
/plasmid="pBeloBACI"
/note="end : SP6"
                                 Location/Qualifiers
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                   pBeloBAC11
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R.Site 2
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uetermination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw Bp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
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clone:MSMg01-271024.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 CTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTG 263
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711 RKRWGTAKATDTGRAAAAAARTAAAGGGGTRTRTRRKRWKWAWAYATATAAGTGWGTAG
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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29.3%; Pred. No. 1;
ttive 77; Mismatches 167; Indels
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                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
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Unpublished
                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7227"
/dlone=lab=RRPOI-98"
/note="end : T7"
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Mus musculus molossinus
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Matches 101; Conservative
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AG411354.1
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohana, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Troukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
PRIMERS
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893 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
046011 of library G from Tetraodon nigroviridis, genomic survey
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etrinopterrygii; Neopterrygii; Teleostei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterrygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Saurin, W. and Weissenbach, J.

Bstimate of human gene number provided by genome-wide analysis using Tetraodon nigrovitidis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 AGGAATGAAAGGGAAAAAAAAAAAAAGGGGGGGGGGGTAAAAATGAAGTGAAGAGGTAGG
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-271024.TJ"
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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: EcoRI
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LIBRARY
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Matches 108; Conserv
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PUBMED

us-09-899-276c-1.rst

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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                    Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="1646011"
/clone lib="6"
/clone lib="Genoscope sequence ID : COBG046AH06LP1~end : T7"
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       Rocet Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of Ereshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 893
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3 (bases 1 to 893)
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Best Local Similarity 43.9%
Matches 190; Conservative
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Submitted (IT-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); I-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp) (Mishttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) (Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-289-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp
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                                                                    Mus musculus molossinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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tori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                             ,M., Toyoda,A., Noguchi,H., Sequences of Library MSMg01
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/sub_species="molossinus"
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/clone="MSMg01-189C10.TJ"
/sex="male"
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Pred. No. 2;
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                   GI:47991140
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llarity 45.9%;
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Direct Submission
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BAC end Sequ
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R.Site 2
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Matches 14
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ut. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                               Drosophila melanogaster genome survey sequence SP6 end of BAC BACNOSCO7 of DrosBAC library from Drosophila melanogaster (fruit ALI), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AATGGTGATGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCGGG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACN09C07"
/clone="bacN09C07"
/plasmid="bBelobBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                               AL102403.1 GI:5614014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBeloBAC11
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RESULT 15
CNS0134P/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                             DEFINITION
                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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Search completed: August 4, 2005, 14:31:57

Job time : 2839.9 secs

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37, Appl 44, Appl 16073, A

Sequence 158 Sequence 155 Sequence 37, Sequence 160 Sequence 160 Sequence 235

Sequence 8 Sequence 8 Sequence 1 Sequence 1 Sequence 1

2, Appli 15273, A 68086, A

Sequence Sequence Sequence

ALIGNMENTS

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US-09-244-796-3
US-09-509-712B-56
US-09-621-976-8976
US-09-949-016-1358B5
US-09-949-016-1358B5
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US-09-949-016-1458B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
TELEPAC: (703)836-9300
TELERA: 89910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 70.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  5.7 277
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IOPOLOGY: linear IMMEDIATE SOURCE:
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US-08-232-463-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
       Query Match
       Sequence 13587, A Sequence 13, Appli Sequence 1678, A Sequence 14150, A Sequence 15648, A Sequence 15648, A Sequence 14001, A Sequence 14001, A Sequence 194028,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16431, A
Sequence 17, Appl
Sequence 17, Appl
Sequence 2813, Ap
Sequence 15094, A
Sequence 1509, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2813, Ap
Sequence 16268, A
Sequence 15841, A
Sequence 18033, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Appl
Sequence 32, Appl
Sequence 3, Appli
                                                                                                                                                      August 4, 2005, 07:01:49; Search time 123.644 Seconds (without alignments) 7940.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Appl
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Sequence 12333,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                1 taggaaaattataggatcat.......6ctggaatcatccatttaaa 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-09-949-016-14150
S-09-949-016-15648
S-09-949-016-14001
S-09-949-016-14002
S-09-949-016-13432
S-09-949-016-13432
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US-09-949-016-15841
US-09-949-016-15841
US-09-049-016-15841
US-09-049-016-15094
US-09-244-796-17
US-09-949-016-15094
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US-09-949-016-16509
US-09-949-016-16678
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US-09-949-016-14001
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US-09-949-016-14001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-244-796-3;
US-09-007-005-3
                                                                                                                                                                                                                                                                                                                                                                                                            1202784 segs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                               US-09-899-276C-1
600
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Match Length
                                                                                                                                                                                                                                                                                                                                          Scoring table:
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35.4
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Length 7218;

DB 1;

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118 WRKKSYRRTRCAWAYAWKTKRSYYWCWRWKWKRCMMMMMMAMAYGKTMMMRACWKTRYWR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15841, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                             Sequence 16268, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 6.6%;
1 Similarity 50.8%;
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88580 CATAT 88576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 94; Conserva
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                                                                                                                             RESULT 3
US-09-949-016-16268/c
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US-09-949-016-16268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 TCATWCYWYWKYWKRWWSKTCWSGSRGGYMTSYTSTRSYSMYWASWMYTMCWWWGRWWST 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 TCCAATGAGGAGGAATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 TIATAGATITITATACATACACAGAGAATACGGACTAGTGAGAAGCTATGCCATGGTCC 364
                                                                                                                                                                                                                                                                                                                                                                                                    305 ITAIAGAITITAIACAIACAGAGAAAIAACGGACTAGIGAGAAGCIAITGCCAIGGICC 364
                                                                                          TTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
                                                                                                                                                                                                                                                                                                                    245 TCCAATGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC 304
                                        ö
                                                                                                                                                                                            125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG 184
                                                                                                                                65 AATGGTGATGATGTACATCAAGCAGGAGAAAACCAAATGAACCAGATGCGAATTCGGG 124
                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AAAATTATAGGATCATTAAGAAAGGAGAAGGAAGGAGGAGGAGCAAATACCTGGAGGTAGA
                                           Gaps
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llarity 10.5%; Pred. No. 0.024;
Conservative 140; Mismatches 125; Indels
                          Similarity 3.3%; Pred. No. 1.4e-11; 13; Conservative 237; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2813, Application US/09621976
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
   APPLICANT: Undert, S. APPLICANT: Jobett, S. APPLICANT: Glordano, U.Y.
; APPLICANT: Glordano, U.Y.
; TITLE REFERENCE: GRNSET.054PR2
; FILE REPERENCE: GRNSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATES: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: :: :: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAAGAGATGATGAAGGCCTAAATATGGA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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LENGTH: 832
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                                        Best Local
Matches 1
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GENERAL INFORMATION:
APPLICAMT: VOTERE, J. Craig et al.
APPLICAMT: VOTERE, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: US/09/949,016
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
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SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESEQ for Windows Version 4.0

LENGTH: 128175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AAGCTATTGCCATGGTCCAAGCAAGAAGATGAAGGCCTAAATATGGAGCCAAAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AGCAATGAAGAATGAGCCATGCAGGGTGAAAATGCTGCATGTTGTAAATGGAGGAAAAGA
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                                                                        58 WWAWAAMWEMWITMPOMYYYWYNEAMKERWMWEKWESWSWMWAWGMITEWAAENWWEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 0.48;
0; Mismatches 91; Indels 0;
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APPLICANT: VENTER, J. Craig et al.
IITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
IITLE OF INVENTION: WITH HUMAN DISSEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12242 AGACAGCAAACCAAAAAAAAGATGGTTAGAATAAATAAGAATTTTACTTAATGATTGCTA 12301
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                           385 CTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCA 444
                                                                                                                  TGTTGTAAATGGAGGAGAAGACCTGTGACTTCAGATATGAAAACCTCATCTTCAACCCA 504
                                                                                                                                         159 GAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGT
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46.5%; Pred. No. 1.5;
ive 0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16431, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09007005B Patent No. 625858 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KEY: misc_feature
| LOCATION: (1)...(16741)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-16431
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Matches 118; Conservative
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76 AAWWWTWA
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US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
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                                                                                                               Score 39.4; DB 4; Length 177251;
Pred. No. 0.57;
0; Mismatches 171; Indels 0;
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APPLICANT: diordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.1%; Score 36.8; DB 4; Best Local Similarity 13.3%; Pred. No. 0.18; Matches 41; Conservative 130; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18033, Application US/09621976
Patent NO. 6639063
GRERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n=a, g, c or
                                                                                                           Query Match
Best Local Similarity 45.4%;
Matches 142; Conservative
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LOCATION: 16
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US-09-621-976-18033/c
                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15841
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LENGTH: 177251
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LENGTH: 474
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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US-U9-244-/20-1)

Sequence 17, Application US/09244796

Sequence 17, Application US/09244796

Sequence 17, Application US/09244796

GENERAL INFORMATION:
APPLICANT: SCOSTAK, AICHARM W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: POSIONS
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/35007
CURRENT APPLICATION NUMBER: 05/09/244,796
CURRENT FILING DATE: 1999-02-05
SARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASESCE for Windows Version 4.0

SEQ ID NO 17

LENGTH: 289
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-0-1-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/044,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-01-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
EBROTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 289;
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Best Local Similarity 4.6%; Pred. No. 0.22;
Matches 9; Conservative 89; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature;

LCCATION: (1)...(289)

CTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 ASARSAKRCCYSCSWGAMSWKYMWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AGAGATAAGTITCAGGAAATGTAACTTATAGAITTTATACATACACAGAGAAATACGGAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 SMWMCWIRSWKYCYIKARWIGYYCYRKGGMWGKRGRWYASKKYMWKRWKWWCWARMYRYST 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 NRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSR 207
                                                                                                                                                                                                                                                                                                                                                                                             88 NRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRN 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTC
                                                                                                                                                                                                                                                                                           28 URURURARCRARARURURARCRARARURGRINRINRSRINRINRSRINRINRSRINRINRSR
                                                                                                                                                                                                                                                                                                                                                              61 TAGAAATGGTGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT
                                                                                                                                                                                                                                                               1 TAGGAAAATTATAGGATCATTAAGAAAGGAGAAGAAGAAGAGTGGGAGCAAATACCTGGAGG
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                                                                                                                                                                       DB 3; Length 289;
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; Sequence 2813, Application US/09621976
; Patent No. 653963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTA and Encoded Human Proteins.
; TITLE OF INVENTION: ESTA and Encoded Human Proteins.
; FILE REFERENCE: GLORET, 054PR.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTUN NO 2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%; Score 36.2; DB 4; Best Local Similarity 13.1%; Pred. No. 0.38; Matches 29; Conservative 102; Mismatches 90;
                                                                                                                                                                                                                        :66
                                                                                                                                                                       Query Match
Best Local Similarity 4.6%; Pred. No. 0.22;
Matches 9; Conservative 89; Mismatches
CTHER INFORMATION: Translation template BATURE:
NAME/KEY: misc feature
COCATION: (1)...(289)
CTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AATGTTAGGGTGAAAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 NRNRSRNRNRSRCRARG 224
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813
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US-09-621-976-2813
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US-09-949-016-16509
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Sequence 15094, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PATILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEATSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16509, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
FATELIANT: VERMER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Verbion 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199177 AGCAATAGAGTGAGACCCTGTCTCAACAAAAAAAAAGTGTTTCCTTTTCAGTCTCAGAT 199236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTACTACTACTCAACTCTGTAGGTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 209210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 36; DB 4; Length 209
47.0%; Pred. No. 7.5;
tive 0; Mismatches 125; Indels

; LOCATION: (1) ... (209210)

; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15094

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Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 15094
LENGTH: 209210
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LENGTH: 174639
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RESULT 12
US-09-328-352-2835/c
| Sequence 2835, Application US/09328352
| Sequence 2835, Application US/09328352
| Patent No. 6562958
| GENERAL INFORMATION:
| APPLICANT: Gary L. Breton et al.
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/328,352
| CURRENT PILING DATE: 1999-06-04
| NUMBER OF SEQ ID NOS: 8252
| LENGTH: 1245
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%309-999-016-13587, Application US/09949016

% Sequence 13587, Application US/09949016

% Patent No. 6812339

% GENERAL INFORMATION:

% APPLICANT: VENTER, J. Craig et al.

% TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

% TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

% CURRENT APPLICATION NUMBER: 2009-04-14

% CURRENT PILING DATE: 2000-04-14

% PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                           25 AAAGGAGAAGAGGAGGAGCAAATACCTGGAGGTAGAAATGGTGATGTGTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 TGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTACTAC
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                                                                                                                                                                                     Gaps
                                                                                                                       DB 4; Length 174639;
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Pred. No. 0.97;
0; Mismatches 88;
                                                                                                                    Score 35.4; DB; Pred. No. 11; 0, Mismatches
LOCATION: (1)...(174639)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Acinetobacter baumannii
US-09-328-352-2835
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ilarity 50.0%;
Conservative (
                                                                                                                       Query Match 5.9%;
Best Local Similarity 49.2%;
Matches 93; Conservative
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Best Local Similarity
Matches 88; Conserv
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RESULT 15
US-09-949-016-16678
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Sequence 3, Application US/09751389

Patent No. 6630334

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION UNMER: US/09/751,389

CURRENT FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 3

LENGTH. 186431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 IGCCAIGTTTAGAGATTCAGAGATAGGTTTCAGGAAATGTAACTTATAGATTTTATACAT 321
                                                                                                                                                                                                                                                                                                                                                                                       7305 İGAĞCAAĞAAĞATGGGİĞİĞGAĞAĞAÇAGAĞAĞAĞTTĞGAGGTĞGAĞAAAAAAAÇA 7246
                                                                                                                                                                                                                                                                                                                                                            310 GATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCCAAGCA 369
                                                                                                                                                                                                                                                                                         250 TGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATACAGAAATGTAACTTATA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTAC
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                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                              73;
                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7185 AGAGAGATGGGGTGGAAAAGAAGAGGAGAAA 7154
                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AGAGATGAAGGCCTAAATATGGAGCCAAA 401
                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.0%; Pred. No. 2.9;
Matches 79; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRASE EXECTION NUMBER: 207012
SOPTWARE: FRASE FOR Windows Version 4.0
SEQ ID NO 13587
LENGTH: 10321
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), LOCATION: (1)...(786431)

), OTHER INFORMATION: n = A,T,C or G

US-09-751-389-3
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ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-13587
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US-09-751-389-3
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                                                                                                                                                                                                              Score 35; DB 4; pred. No. 9.7; pred. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            4, 2005, 14:40:33
Sequence 16678, Application US/09949016
                                                                                                                                                                                                                 5.8%;
Dest Local Similarity 55.3%;
Matches 68; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                Search completed: August
Job time : 128.644 secs
                                                                                                                                                                                                                                                                                                                                    326 AGA 328
                                                                                                                                                                                                                                                                                                                                                      615 AAA 617
                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16678
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August 4, 2005, 08:04:16; Search time 1070.28 Seconds (without alignments) 3633.986 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ជ	1, Appli	4, Appli	Sequence 112, App	13, Appl	170737,	Sequence 170737,	742, App
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	ID	9 US-09-899-276-1	US-10-685-705-4	US-10-085-117-112	US-10-275-323A-13	US-10-027-632-170737	US-10-027-632-170737	US-10-087-192-742
	038	6	19	17	21	13	17	13
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æ	Query Match	100.0	100.0	7.1	7.0	7.0	7.0	6.9
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		40 36 36	10	US-10-221-714A-391 US-10-027-1632-190233 US-10-027-632-190233 US-10-22-115-17130 US-10-240-445-1099 US-10-312-841-2 US-10-027-632-161407	Sequence 391, 2 Sequence 19023, Sequence 19023, Sequence 17173 Sequence 2, M Sequence 16140 Sequence 16140	391, App 1630, Ap 190233, 190233, 17730, 1099, Ap 12, Appli 161407,

JS-09-899-276-1

JOHENTALIA INTEGRATION:

JAPPLICANT: Soto, Ubaldo

JAPPLICANT: Soto, Ubaldo

JAPPLICANT: Soto, Ubaldo

JAPPLICANT: Soto, Ubaldo

JAPPLICANT: Patrick

APPLICANT: Poustka, Annemarie

JAPPLICANT: Delius, Hajo

JAPPLICANT: Dur Hausen, Harald

APPLICANT: Patzelt, Andreas

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JAPLICANT: Patzel Gaps ö Length 600; 100.0%; Score 600; DB 9; Length 60 100.0%; Pred. No. 9.6e-167; ative 0; Mismatches 0; Indels Sequence 1, Application US/09899276 Patent No. US20020106355A1 GENERAL INFORMATION: Query Match Best Local Similarity 100. Matches 600; Conservative ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-899-276-1

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48511 GAACTGTGAATCTCCAGGCACAGCAGGAGGGGGGTCAACCATACAGTGATAAGAAAT 48452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCAAGGAAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGGAGCAATGAAGAATG
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<u>AATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT</u>
                                                                                  Sequence 112, Application US/10085117
Sequence 112, Application US/10085117
FUDIcation No. US20030232334A1
GENERAL INFORMATION:
APPLICANT: Bngelhard, Eric K.
APPLICANT: Bngelhard, Eric K.
TILLE OF INVENTION: VOVEL COMPOSITIONS AND METHODS FOR CANCER
TILLE REFERENCE: 529452000121
CURRENT PELING DATE: 2002-02-27
CURRENT FILING DATE: 2002-02-27
FRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112
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ORGANISM: Homo sapiens
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US-10-085-117-112/c
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APPLICANT: University of Kentucky Research Foundation
APPLICANT: JANAKAISHNA, Ambati
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APPLICANT: UNIVERSITY Set of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of transport of tra
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                                                                                                            Length 11793;
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100.0%; Score 600; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-166;
Matches 600; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10685705
Sequence 4, Application US/10887A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-685-705-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 TGAGTCAAGGGATTTGAATGTTAGGGTGAAAGTTACTACTCCAACTCTGTAGGTTAAAAG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 TRDDHBRHDHHRTKHDWYNKKWHDGWHKHKHVRVNDDWDBVWNRDDWRRSRNRWTWDDD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AGAAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAG 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 DWWDHWDAWYDGHKRAARWHYDYTGGTTKHRTTYNKDDDKYSYRDRRRWWRYRSWDRRWT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 GACCTGTGACTTCAGATATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 GAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGA
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US-10-275-323A-13
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LOCATION: (357)...(357)
OTHER INFORMATION: a, c, g, or
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                                                                                                                                                                        NAME/KEY: modified base
LOCATION: (324)..(324)
OTHER INFORMATION: a, c, g,
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LOCATION: (330)..(330)
OTHER INFORMATION: a, c, g,
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LOCATION: (364)..(364)
OTHER INFORMATION: a, c, g,
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INFORMATION: a, c, g,
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48 GYGGANRKRRCMWY 35
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LOCATION: (355)..(355)
OTHER INFORMATION: a, c,
NAME/KEY: modified base
LOCATION: (253)..(253)
OTHER INFORMATION: a, c,
                                                                                                         LOCATION: (269)..(269)
OTHER INFORMATION: a, C,
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LOCATION: (352)..(352)
OTHER INFORMATION: a, c,
                                                                                      NAME/KEY: modified base
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APPLICANT: LAUDET, VINCENT
APPLICANT: LAUDET, VINCENT
APPLICANT: LAUDET, VINCENT
APPLICANT: LAUDET, VINCENT
APPLICANT: HANNI, CATHERINE
APPLICANT: HANNI, CATHERINE
APPLICANT: HANNI, CATHERINE
APPLICANT: HANNI, CATHERINE
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: UNMER: US/10/275,323A
CURRENT APPLICATION NUMBER: US/10/275,323A
CURRENT APPLICATION NUMBER: FT 00/05850
PRIOR APPLICATION NUMBER: FR 00/05850
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATERIAL VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: DNA fragment amplified OTHER INFORMATION: from the genome of birds
                         48391 CTATCCTGTTGGCAAAAGAGA 48371
                                                                                                                                               Sequence 13, Application US/10275323A Publication No. US20050079491A1 GENERAL INFORMATION:
206 CAACTCTGTAGGTTAAAAGGA 226
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LOCATION: (245)..(245)
OTHER INFORMATION: a, c, g, or t
FEATURE:
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LOCATION: (134)..(134)
OTHER INFORMATION: a, c, g,
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LOCATION: (43)..(43)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c,
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OTHER INFORMATION: a, c,
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LENGTH: 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 GGAGAAAACCAATGAACCAGATGCGAATTCGGGCCCACACCAATGTCAAGGGATGACAAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 AAGGAAGAGTGGGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATCAAGCAG 91
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,218
FRIOR APPLICATION NUMBER: US 60/185,218
                                                                                      SERNEMAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.1.29

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/01/08,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-03-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FREEEGQ for Windows Version 4.0

LENGTH: 760

LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 41.8; DB 13;
50.2%; Pred. No. 0.13;
tive 0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 TGTAGGTTAAAAGGAAACGTTGAGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170737, Application US/10027632 publication No. US20030204075A9 GENERAL INFORMATION:
                   Sequence 170737, Application US/10027632 publication No. US20020198371A1 GENERAL INFORMATION:
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Best Local Similarity 50.2
Matches 103; Conservative
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US-10-027-632-170737
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US-10-027-632-170737
RESULT 5
US-10-027-632-170737
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9409 AGGCACAAGGAACAGCAGCTACAAAGGCTCGGAAGGGTCGGAATGAACTTAATGTGTTCACA 9468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 TAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTACTACTCAACTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 gagagagaangaangaangaangaantigaattititigaactaacaaaaaanataaca 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 GGAGAAAACCAATGAACCAGATGCGAATTCGGGCCCACACCAATGTCAAGGGATGACAAT 151
                                                                                                                                                                                                                                                                                                                                                                                                             32 AAGGAAGAGTGGGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATCAAGCAG
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Squence 742, Application US/10087192
Squence 742, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MORTIS, David W.
APPLICANT: MORTIS, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADACRE US/10/087,192
CURRENT APPLICATION NUMBER: US/09/747,377
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE FRASESEQ for Windows Version 4.0
SEQ ID NO 742
LENGTH: 78268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCGGGCCC 127
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 102;
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Best Local Similarity 62.7%; Pred. No. 1.6;
Matches 64; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          0.13;
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FABESEQ for Windows Version 4.0
SEQ ID NO 170737
                                                                                                                                                                                                                                                                                                                                Score 41.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 TGTAGGTTAAAAGGAAACGTTGAGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      736 GAATGAGTTAAGTGAGGAGGTGGGA 760
                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%;
Best Local Similarity 50.2%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo sapiens
US-10-087-192-742
                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170737
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FEATURE: OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence : 216681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/10304019
Publication No. US20040102622A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
FILE REFERENCE: PTS-0043
CURRENT PAPLICANT: 2002-11-23
NUMBER OF SEQ ID NOS: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88137 ATCAATTCAAAGAGAGTCTGGCATAAAGAAAGCTGTGTGTAAAGGAGGCAGGACAAAAA 88078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AGTTTCAGGAAATGTAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 CATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTTGGGGCCCACACAATGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AAGAAAGGAGGAAGAGGAGGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AGCAATGAAGAATGAGCCATGCAGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGA
                                                                                                                                                                       OTHER INFORMATION: Distance between a terminus base of telomere on OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base OTHER INFORMATION: sequence : 28899985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.6; DE Pred. No. 0.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.4; Di
Pred. No. 6.8;
0; Mismatches
                                                                                         FEATURE:
OTHER INFORMATION: Located on chromosome 16
                                                               OTHER INFORMATION: HUMUT8173B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.64;
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Best Local Similarity 51.7%;
Matches 90; Conservative
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Best Local Similarity 50.8
Matches 94; Conservative
           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88077 CATAT 88073
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                                                                                                                                             FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         US-10-674-124A-22067
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US-10-304-019-12/c
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: 55607-55706, 360227-360326, 363103-363202, 363428, 366093-366192,
LOCATION: 368528, 447324, 45253-452752, 457192, 457207-457306, 461808-461907,
LOCATION: 461921, 461928, 461942
OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512227 AGGTGGTGGTAAGCTATTTGGATTATATTAAAGCAAATTGGGCAGCCACTGAAAAAATG 512286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512287 Gagadadaaaargirarararararararararrirraaaaargiaacrcagarricaa, 512346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512407 AGAGGTGATGCTTGCCTAATCAAGAATGGTAGCAGGAGGAAGTGAGGAAGTGGACCGAT 512466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 AGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC-----TTATA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GATITIATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCCAAGCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 AGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAGCCATGCA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512467 GTGTAATATTTCTGTAGGTGAAATAGATGATGATGATGATAAATTAGATGGGGGA 512523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 GGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGATATGAA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 599001;
Sequence 4, Application US/10317869A
Publication No. US20050101000A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 4B EXPRESSION
FILE REFERENCE: TRS-0429
CURRENT APPLICATION NUMBER: US/10/317,869A
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 4
LENGTH: 599001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TAMIXA, GENE MAPPING METHOD USING MICROSATELLITE TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS; FILE REFERENCE: ORIN-003CIP 9.7 (CURRENT APPLICATION NUMBER: US/10/674,124A; CURRENT FILING DATE: 2003-09-26; PRIOR APPLICATION NUMBER: 10/257,511 PRIOR APPLICATION NUMBER: 10/257,511 PRIOR APPLICATION NUMBER: PCT/JP00/07621 PRIOR APPLICATION NUMBER: DFCD00-112699 PRIOR FILING DATE: 2000-04-13 PRIOR FILING DATE: 2000-04-13 PRIOR FILING DATE: 2000-04-13 PRIOR FILING DATE: 2000-04-13 PRIOR FILING DATE: 2000-04-13 PRIOR FILING DATE: 2002-01-209-28 PRIOR FILING DATE: 2002-12-09

PRIOR FILING DATE: 2002-12-09

PRIOR FILING DATE: 2002-12-09

SEQ ID NO 22067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.8; DB 21; Length
Pred. No. 10;
0; Mismatches 147; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.5%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INOKO, Hidetoshi
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-674-124A-22067
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Sequence 322, Application US/10087192
Publication No. US20020182586A1
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Squance 12, Application US/11013608
Squance 12, Application No. UG2005015325A1
GURBEAL INFORMATION
SQUANCE 12. Frank
APPLICANT: Great Ponnia
APPLICANT: Wicholas M. Dean
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Marc
APPLICANT: All M. Cowert
APPLICANT: Lax M. Cowert
APPLICANT: Lax M. Cowert
APPLICANT: Lax M. WORSEN: William A. Gaarde
APPLICANT: Lax M. WORSEN: William A. Gaarde
APPLICANT: Lax M. WORSEN: US/11/013.608
FILE REFERENCE: BNDL-000905. Pl
CURRENT FILING DATE: 2004-112-16
FRIOR FILING DATE: 2002-11-12
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FRIOR FILING DATE: 2002-11-1
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Best Local Similarity 50.8%; Pred. No. 6.8%
Matches 94; Conservative 0; Mismatches 91; Indels 0; (
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RESULT 12 US-10-087-192-322/C

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; Sequence 263881, Application US/10027632
; Publication No. US20020198371A1
; Publication No. US20020198371A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G,
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: DAVISER: US/0007-12
; FILE REFERENCE: 108827.129
; CURRENT PELLING DATE: 2002-04-30
; PRIOR PELLING DATE: 2000-07-12
; PRIOR PELLING DATE: 2000-04-20
; PRIOR PELLING DATE: 2000-04-20
; PRIOR PILLING DATE: 2000-04-20
; PRIOR PILLING DATE: 2000-03-24
; PRIOR PILLING DATE: 2000-02-24
; PRIOR PILLING DATE: 1090-11-23
; PRIOR PILLING DATE: 1999-11-23
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; PRIOR PILLING DATE: 1999-11-23
; PRIOR PILLING DATE: 1999-11-23
; PRIOR PILLING DATE: 1999-09-28
; PRIOR PILLING DATE: 1999-108-09
; PRIOR PILLING DATE: 1999-09-08
; PRIOR PILLING DATE: 1999-09-08
; PRIOR PILLING DATE: 1999-09-08
; PRIOR PILLING DATE: 1999-09-08
; PRIOR PILLING DATE: 1999-08-09
; ROPIWARR: FRAESEQ for Windows Version 4.0
; SEQ ID NO 263881
; LENGTH: 3918
; TANDAR
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PUBLICATION NO. US20020182586A1

PUBLICATION NO. US20020182586A1

GENERAL INFORMATION:
APPLICANT: MORTIS, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR PELICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-10-03-05

NUMBER OF SEQ ID NOS: 2059

SOUTHARE FRALESTED FOR WINDER: US 09/798,586
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50.8%; Pred. No. 7.2;
tive 0; Mismatches 91;
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Best Local Similarity 50.00.
These 94; Conservative
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CRGANISM: Homo sapiens
US-10-087-192-322
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LENGTH: 144035
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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FRIOR PELICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
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FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/167,363
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Publication No. US20030204075A9
CENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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14.1%; Pred. No. 1.6;
ve 0; Mismatches 33; Indels 0;
                                                                                         Length 3918;
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                                                                                   Score 39.2; DB 13;
Pred. No. 1.6;
0; Mismatches 33;
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GENERAL INFORMATION:
                                                                                Query Match
Best Local Similarity 64.1%;
Matches 59; Conservative
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Best Local Similarity 64.1<sup>3</sup>
Matches 59; Conservative
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US-10-027-632-263881/c
; ORGANISM: Human
US-10-027-632-263881
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US-10-027-632-263882
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376 ATAGAGGCAGGAAGACAATTAGGAAGCCATTGCAATCATCCAAGTGAGAGGTGCTGAATG 317
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PRIOR FILING DATE: 1999-10-34
PRIOR FILING DATE: 1999-108-18
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
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Matches 59; Conservative
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US-10-027-632-263881
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LENGTH: 3918
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PAT 01-FEB-2002
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AR30620 Sequence
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CQB11706 Sequence
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CQ775689 Sequence
BD195643 70 human
CQ775689 Sequence
BD195643 70 human
CQ775689 Sequence
AR322698 Sequence
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AR559317 Sequence
BD080551 Chemokine
S69738 MCP-1=monoc
X60011 Heapiens g
G06615 human STS W
A37281 Sequence
AX311515 Sequence
AX363653 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  monocyte ch
MCP-1 mRNA.
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Sequence 2 from Patent EP1170372.
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CQ831706

BD195644

CQ775689

BD195643

CQ775688

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HUMMCHEMP

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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells

Patent: WO 015/278-A 5501 09-AUG-2001;
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                                                        1 TGCAGCIAACTIATTTTCCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATATATG
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Score 198.4; DB 9;
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0; Mismatches 1;
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LOCUS CQ096880 Brom Patent W00157272.
DEFINITION Sequence 5739 from Patent W00157272.
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Sequence 5501 from Patent WO0157278.
CQ069701
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Location/Qualifiers
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      Query Match
Best Local Similarity 99.5%;
Matches 199; Conservative
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7686. 8467
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                                                                                             PRI 18-OCT-2000
                                                                                                                                                                                                                                                  Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Rosl, F.
Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic than positive cells: the role of the chromatin structure and AP-1 composition

Oncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Newenheimer Feld 506, 69120
Heidelberg, FRG
Location/Qualifiers
                                                                                                                                                                                                        Eukaryoja, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="MCP-1"
/codon_start=1
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Homo sapiens (human)
Homo sapiens
                                                                                                  HSY18933 107-1 gene and enhancer region. Y18933 1 GI:10933860
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PAT 21-JAN-2004 168 61 AATTITGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTA 120 121 TTGATGITITAAGITTAATCITICATGGTACTAGTGTTTTTAGATACAGAGACTTGGGGA 180 linear

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/db_xref="taxon:9606"
/note="MAP TO AC005549.1~EXPRESSED IN HEART, SIGNAL = 2.6"
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                                                                  61 AATTITGITIGITGATGIGAACATTAIGCCTTAAGTAAIGTTAATTCTTATTTAAGTTA 120
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                   227 IGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCCCTGTTTTATTTTATAATG
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 1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTTATTTTTATAATG
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0152274-A 5454 09-AUG-2001;
Aeomica, Inc. (US)
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Sequence 5454 from Patent W00157274.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005549.1~EXPRESSED IN BONE MARROW, SIGNAL
= 2.4"
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                                           Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Patent: WO 0157276-A 5703 09-AUG-2001;
Acomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157222-A 5739 09-AUG-2001;
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larity 99.0%; Pred. No. 4.3e-26;
Conservative 0; Mismatches 2; Indels 0
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                 GI:41065906
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CQ135681.1 GI:41093047
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CQ096880
CQ096880.1
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Matches 198; Conserv
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TGCAGCTAACTTTTTCCCCTAGCTTTCCCCCAGACACCCTTGTTTTATTATAAATG
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                             Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER.130 DB 0004 WO
3.4150. US 60/180, 312-151> 04 February 2000 (14.02.00).015-150 US
60/207, 456-151> 26 May 2000 (26.05.00).6150> US 09/632,366-151> 03
AUGUST 2000 (03.08.00).6150> US 60/234,857-151> 27 September 2000
(27.09.00).150> US 60/234,857-151> 21 September 2000
(27.09.00).6150> US 09/608,408-151> 30 June 2000 (30.06.00).6170>
MOlecular Dynamics Sequence Listing Engine
MOlecular Dynamics Sequence Listing Engine
Acomica, Inc. (US)
Acomica, Inc. (US)
1. 360
/ Organism="Homo sapiens"
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1. .50

/organism="Homo sapiens"

/mol type="unassigned DNA"

/db_xref="taxon:9606"

/nore="MAP TO AC005549.1~EXPRESSED IN PETAL LIVER, SIGNAL

= 3.7"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 4.3e-26;
0; Mismatches 2;
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Matches 196
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                         TTGATGITTTAAGTTTATCTTTCATGGTACTAGTGTTTTTAGATACAGAGACTTGGGGA
                                                                                                                      1. .360 /organism="Homo sapiens" /mol type="unassigned DNA" /mol type="unassigned DNA" /mol type="texon:9606" /noce="MAP TO AC005549.1~EXPRESSED IN LUNG, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human lung
Patent: WO 0186003-A 5889 15-NOV-2001;
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98.4%; Score 196.8; DB 6;
Best Local Similarity 99.0%; Pred. No. 4.3e-26;
Matches 198; Conservative 0; Mismatches 2;
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PAT 08-OCT-2004
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Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
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Charge tags and separation of nucleic acid molecules
Patent: WO 02063030-A 72 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
1. . 647
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326 IGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCCTGTTTTATTATTATATGT
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Pred. No. 3.8e-26;
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other sequences; artificial sequences.
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Patent: US 6780982-A 72 24-AUG-2004;

    647
    organism="unknown"
    /mol_type="unassigned RNA"

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Sequence 72 from Patent W002063030.
AX698741
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Coganism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="texon:9606"

/note="MAP TO AC005549.1~EXPRESSED IN BRAIN, SIGNAL = 2.5"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
Patent: WO 2004072265-A 294 26-AUG-2004;
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
33._199
/note="Each #n# represents a nucleotide selected from t, g or c, or contains no nucleotide."
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                                               Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human brain
Patent: WO 0157275-A 5534 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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98.4%; Score 196.8; DB 6; Length 360;
Best Local Similarity 99.0%; Pred. No. 4.3e-26;
Matches 198; Conservative 0; Mismatches 2; Indels 0
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CQ861661.1 GI:51982650
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I (bases 1 to 725)
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Immuno-Demo,A. and DeVico,A.L.
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                                                                                     /mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Unknown.
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Cooksostitions for the detection of blood cell and immunological compositions for the detection of blood cell and immunological response gene expression
Fatent: US 6607879-A 1344 19-AUG-2003;
Patent: US 6607879-A 1344 19-AUG-2003;
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/ organism="unknown"
/ mol_type="genomic DNA"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			d			SUMMARIES	
Result No.	ult No.	Score	Query Match	Query Match Length DB	DB	Ϊ́Ď	Description
	-	200	100.0	200	9	ADH13939	Adh13939 Human mon
	~	198.4	99.2	489	σ	ACH19135	Ach19135 Human adu
	٣	198.4	99.2	772	13	ADS16434	Ads16434 Human cyt
υ	4	198.4	99.2	1005	10	ADI02670	Adi02670 Human cDr
O	ß	198.4	99.2	1472	10	ADE25637	Ade25637 Human cDl
	9	198.4	99.5	11793	12	ADO03803	Ado03803 Human Cc
	7	198	99.0	950	æ	ACF64400	Acf64400 Human MCP
	8	197.6	98.8	2775	9	ABK47979	Abk47979 Human sma
υ	σ	196.8	98.4	360	4	AAI15568	Aai15568 Probe #55
O	10	196.8	98.4	360	4	ABA57500	Aba57500 Human foe
υ	11	196.8	98.4	360	4	AA137053	Aai37053 Probe #57
υ	12	196.8	98.4	360	4	ABA26988	Aba26988 Probe #54
υ	13	196.8	98.4	360	4	AAK31146	Aak31146 Human bon
U	14	196.8	98.4	360	4	AAK05543	Aak05543 Human bra
υ	15	196.8	98.4	360	4	ABS30826	Abs30826 Human liv
U	16	196.8	98.4	360	9	ABS05898	
	17	196.8	98.4	508	13	ADR52943	Adr52943 Drug thes
	18	196.8	98.4	647	9	ABS68800	Abs68800 Human mon
	19	196.8	98.4	725	~	AAQ85370	Aag85370 Chemoattr
	20	196.8	98.4	725	~	AAX80631	Aax80631 Monocyte

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	Add18494 Human pro		Adi32018 Human cDN	Adr05375 Human mon	Aan91337 DNA which	Aav10341 cDNA enco	Abv78071 Hypoxia-r	Abz34738 Coding se	Adf45446 Human vas	Adn04745 Antipsori	Adr24988 Breast ca	Adp24778 PRO polyp	Aaa34899 Human ade	Aaf21021 Human low	Abz96715 Human nuc	Adi31839 Human cDN	Abd20564 Human pul		Adi02669 Human cDN	Add14996 Human mon	Adn95635 Human BEC	Ado03800 Human Cc1	Adp75913 Human SCY	Adq76211 Chemokine
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21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention mas cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:2. Poustka A; Delius H, Disclosure; SEQ ID NO 2; 30pp; English. Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. ADH13939 standard; DNA; 200 BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. EP1170372-A1. Homo sapiens 09-JAN-2002. ADH13939; ADH13939 ID ADH1 

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09-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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                                                                                                                   AATTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTTTTAAGTTA
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                                                 Sequence 200 BP; 48 A; 29 C; 31 G; 92 T; 0 U; 0 Other;
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                                                                    ; DB 6;
1.5e-30;
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genome mapping; biodiversity; genetic disorder.
                                                                    ; Score 200; DB
; Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stache-Crain
                                                                                                                                                                                                                                         AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                                                                                                          BP.
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                                                                     100.0%;
                                                                                                                                                                                                                                                                                           ACH19135 standard; cDNA; 489
                                                                                                                                                                                                                                                                                                                                                  Human adult lung cDNA #138
                                                                                                                                                                                                                                                                                                                                13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRMANAC R T.
LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                Best Local Similarity 100.
Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense DNA or RNA
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                               ACH19135;
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(LABA/)
(STAC/)
(DICK/)
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                                                                        Query Match
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are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nuclectide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antiSense base of RNA. The purified polypeptide is useful for generating antiSense base of the Tr. The present sequence is useful for generating antiDodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. Language and the province of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
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                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 198.4; DB 9 99.5%; Pred. No. 3.1e-30;
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160. .369
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142. .369
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73..141
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Query Match
Best Local Similarity 99.5
Matches 199; Conservative
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The invention relates to a new combination which comprises cDNAs or their complements not given in the specification that are differentially expressed in vascular endothelium. The combination of cDNAs is useful for preparing a composition for diagnosing or treating vascular disorder, comprising atherosclerosis, haemangioma, haemangioendothelioma, oedema, diabetic retinopathy, warts, pyogenic granulomas, Kaposi's sarcoma, scar keloids, pallergic oedema, neoplasms, psoriasis, ulcers, follicular cysts, endometriosis, periconeal sclerosis or obesity. The present sequence represents a cDNA differentially expressed in the vascular endothelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                  New combination comprising cDNAs that are differentially expressed in vascular endothelium, useful for preparing a composition for diagnosing or treating vascular disorder, e.g., atherosclerosis, psoriasis, ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 88; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1005 BP; 318 A; 183 C; 178 G; 326 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 198.4; DB 10
Pred. No. 3.1e-30;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 211; 28pp; English
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ADE25637 standard; cDNA; 1472 BP.
                                                                                                       Cocke
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Best Local Similarity 99.5°
Matches 199; Conservative
                                                                                                       Bandman O,
                 (BAND/) BANDMAN O. (COCK/) COCKS B G.
                                                                                                                                              WPI; 2003-898115/82
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                                                                                                     Astromoff A,
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ADE25637/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     577
                                                                                                                                                                                                                                                                New isolated human JE cytokine DNA and polypeptide, useful for treating bacterial and viral infections, anemia, or B cell or T cell deficiencies, or in wound healing and related tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid sequence encoding human cytokine, JE. JE sequence is useful in pharmaceutical preparations for stimulating and/or enhancing immune responsiveness, wound healing and related tissue repair. It is also useful for treating bacterial and viral infections, anaemia or B/T cell deficiencies. The present sequence is human JE cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se; vascular endothelium; vascular disorder; atherosclerosis; haemangioma; haemangioendothelioma; oedema; diabetic retinopathy; wart; pyogenic granuloma; Kaposi's sarcoma; scar keloid; allergic oedema; neoplasm; psoriasis; ulcer; follicular cyst; endometriosis; peritoneal sclerosis; obesity; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 772 BP; 239 A; 175 C; 134 G; 224 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.2%; Score 198.4; DB 13; Length Best Local Similarity 99.5%; Pred. No. 3.1e-30; Matches 199; Conservative 0; Mismatches 1; Indels
                                                                                        (DAND ) DANA FARBER CANCER INST INC. (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1; 8pp; English
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89US-00351008.
91US-00701515.
93US-00003136.
94US-00228931.
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                                                                                                                        ) GENETICS INST INC
                                                                                                                                                             Rollins BJ, Stiles CD,
                                                                                                                                                                                                     2004-632933/61
                                                                                                                                                                                                                           P-PSDB; ADS16435
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                 16-MAY-1991;
12-JAN-1993;
13-APR-1994;
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ADI02670/ RESULT

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Gaps

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Kaser MR;

Porter JG,

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Shiffman

Mikita T,

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The invention relates to a combination comprising several polynucleotides chaving any one of 127 sequences (S1) such as the sequence of human CC chaving any one of 127 sequences (S1) such as the sequence of human calmodulin gene, human mRNA for KIAA0930 protein, leukotriene AA calmodulin gene, human mRNA for KIAA0930 protein, leukotriene AA calmodulin gene, human CGI-142 protein mRNA, human KF channel beat 2 subunit by culture and a library of mucleic acid obtaining an expression vector containing the moleic acids, a host cell cortaining the vector, a purified polypeptide appearing as ADE2750 and containing the vector, a purified polypeptide appearing as ADE2750 and ADE2571, producing a protein by culturing the host cell, and a ADE2751, producing a protein by culturing the nost cell, and a ADE2751, producing a protein by culturing the operation of increased nucleic acids are useful for comparison of differential expression of one or more throughput detection of differential expression of one or more throughput detection of differential expression of one or more throughput screening of allibrary of molecules or compounds to comparison with a standard defines early, mid or late atherosclerosis and comparison with a standard defines early, in throughput screening of allibrary of molecules or compounds to identify a ligand which binds a polynucleotide. The library of molecules or compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand from a sample for making a antibody. The protein form a making a making cardiovascular disorder. The foam cell-expressed nucleic acids are useful cardiovascular disorder. The foam cell-expressed nucleic acids are useful cardiovascular disorder. The foam cell-expressed nucleic acids are useful cardiovascular disorder. The presen
                                                                Combination containing several polymucleotide that are differentially expressed in foam cells and complements of the polymucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 41; 37pp; English.
WPI; 2003-875398/81.
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288
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                             rgcaggraactraptriccccquagcrificcccagacacccrigitriarriarrarg
            Gaps
Score 198.4; DB 10; Length 1472;
Pred. No. 3e-30;
0; Mismatches 1; Indels 0;
                                                                                              AATTGCTTTTCCTCTTGTAC 200
    99.2%;
                 Conservative
         Best Local Similarity
Matches 199; Conserv
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Human Cc12 gene and enhancer region DNA SeqID 4.

12-AUG-2004 (first entry)

SEXEXEXEX

AD003803 standard; DNA; 11793

AD003803 RESULT

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91S9 AATTTTGTTTGTTGAAGATTATGCCTTAAGTAATGTTAATTGTTATTTAAGTTA 9218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGATGITITIAAGITITATCITTCATGGTACTAGTGTTTTTTAAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, Ccr2-deficient and/ or a Cc12-deficient (Ccr2-deficient dual Micokout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipotuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and accordingly, such compositions exhibit ophthalmological activities and the human CC12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                          Testing candidate drug for treating age-related macular degeneration, by administering drug to Col2-deficient, Cor2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 rechectivactivatititiccccindectiticcccadacacerticititiatianaare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 198.4; DB 12; Length 11793;
Pred. No. 3e-30;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MCP1 nucleotide sequence >MCP1_03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                                                                                     (KENT ) UNIV KENTUCKY RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF64400 standard; DNA; 950
                                                                                                                                                                                                                                   30-OCT-2002; 2002US-0422096P.
                                                                                                                                                                                                  16-OCT-2003; 2003WO-US032933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.5
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                       WPI; 2004-400512/37.
                                                                                                                                                                                                                                                                                                                                                                                                                               accumulation in eye.
                                                                                                                                     WO2004041160-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2003
                                                                                                       Homo sapiens
                                                                                                                                                                        21-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9279
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                                                                                                                                                                                                                                                                                                              Ambati J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACF64400
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                                                                                                                                                                                                                                                                                                        The present invention describes an isolated polynucleotide (PN) comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising at least 15 contiguous nucleotides of a sequence comprising the requences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN)s comprising two or more of the isolated (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed on a data processing system. The '(PN) can be used for detecting loci associated with multiple sclerosis, ACF64025 to ACF64424 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTTTGTTTGTTTGAAGGAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGAIGITITIAAGITITATCITICATGGTACIAGIGITITITIAGATACAGAGACITIGGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
          detection; computer-readable storage medium; polymorphic site; carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                    polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTTATTATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGATETTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences used in the exemplification of the present invention
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                                                                                                                                                                                                         Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%; Score 198; DB 8; Length 950; 99.0%; Pred. No. 3.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 950 BP; 255 A; 220 C; 184 G; 290 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human small inducible cytokine A2 (SCYA2) genomic DNA
                                                                                                                                                                                                        Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                        Rienhoff HY,
                                                                                                                                                                                                                                                                                      Disclosure; Page 75; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTGCTTTTCCTCTTGAAC
                                                                                                                                                07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK47979 standard; DNA; 2775
                                                                                                                         07-AUG-2002; 2002WO-US025268
                                                                                                                                                                                                       White R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.0
Matches 198; Conservative
                                                                                                                                                                                                                            WPI; 2003-268196/26.
                                                                                                                                                                                (DNAS-) DNA SCI INC
                                                                                                                                                                                                       Jones HB, Xu H,
                                                                            WO2003014319-A2
                                                        Homo sapiens.
                                                                                                   20-FEB-2003
                                                                                                                                                                                                                                                                sclerosis
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          Human;
signal
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The invention relates to single nucleotide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polypeptide. A method for haplotyping the SCYA2 gene in an individual comprises identifying the modelide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the SCYA2 haplotypes given in the specification or whether both copies are defined by applotype pair. Copies are defined by a haplotype pair of the SCYA2 applotype pairs can be assigned to specific genotypes. An association between a contain and a haplotype or haplotype pair of the SCYA2 gene can be cidentified by comparing the frequency of the haplotype or haplotype pair of the SCYA2 agene can be contained to a reference population, where a higher haplotype containty pair in a reference population, where a higher haplotype containty pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2 and in screening for thuman SCYA2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2) gene, useful for studying the function of SCYA2, and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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haplotyping, atherosclerosis, antiarteriosclerotic, gene therapy; single nucleotide polymorphism; genotyping; drug screening; chromosome 17q11.2-q21.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee HH
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Pred. No. 4.3e-30;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                    /product= "Human SCYA2"
                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001WO-US026899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2000; 2000US-0228496P.
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                                                                                                                                                                                                                                                           598. .2080
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Best Local Similarity 98.5
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anastasio AE, Finkel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-339655/37.
P-PSDB; AAU77179.
                                                                                                                                                                                                                                                                                                                                                                                WO200218413-A2
                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTTGTTTGTTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

98.4%; Score 196.8; DB 4;
Best Local Similarity 99.0%; Pred. No. 6.4e-30;
Matches 198; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 5501; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
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2286 AATTGCTTTTCCTTGAMC 2305
                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0227455P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000670
                                                                    DNA; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53
                                                                                                                      (first
                                                                                                                                                                                      cervical cancer; ss
                                                                  AAI15568 standard;
                                                                                                                                                                                                                                          WO200157278-A2.
                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                  Probe #5501
                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                       12-OCT-2001
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                                                                                              AA115568
                                                       AA115568/c
                                            RESULT 9
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTITGTITGTITGATGTGAACAITATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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Pred. No. 6.4e-30;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 5805; 639pp + Sequence Listing; English.
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                                                                                                                                                   Human foetal liver single exon nucleic acid probe #5805.
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            28
                                                                                                                                                                                                                                                                                                                         26-MXY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632468.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
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                                                                             BP
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Best Local Similarity 99.0%;
Matches 198; Conservative
47 AATTGCTTTTCCTCTTGAAC
                                                                                                                                                                                                                                                                                                                2000US-0180312P.
                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000669
                                                                              DNA; 360
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                                                                                                                                 (first
                                                                       7500/c
ABA57500 standard;
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                                                                                                         ABA57500;
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                                                                      ABA57500/
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BP.

(first entry)

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Probe #5454 for gene expression analysis in human heart cell sample.
ABA26988 standard; DNA; 360
                                                                                                                                                Homo sapiens.
                                                23-JAN-2002
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                        ABA26988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTTGGGGA
                                                                                                                       to measure gene expression in human placenta sample.
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                                                                                                                                              microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 5739; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression in human placenta.
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                                             AAI37053 standard; DNA; 360 BP.
                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                       ; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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                                                                                              (first entry)
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Matches 198; Conservative
                                                                                                                                                         genetic disorder; ss.
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                                                                                                                    Probe #5739 used
                                                                                                                                                                                                          WO200157272-A2.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                   09-AUG-2001
                                                                      AAI37053;
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                                                                                                                                              Probe;
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ABA26988/c
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and form and proposing disease, note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
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Human, gene expression, heart, microarray, vascular system, probe, cardiovascular disease, hypertension, cardiac arrhythmia; congenital heart disease, ss.
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99.0%; Pred. No. e...
0; Mismatches
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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AAK05543 standard; DNA; 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 5703; 658pp + Sequence Listing; English.
                                                                                                                                                                                  Human bone marrow expressed single exon probe SEQ ID NO: 5703.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-0236359P.
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                                                                               AAK31146 standard; DNA; 360
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                                                                                                                                                        (first entry)
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                                                 RESULT 13
AAK31146/c
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RESULT 14 AAK05543/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AATTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human brains.
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Pred. No. 6.4e-30;
0; Mismatches 2; Indels 0;
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                            expressed single exon probe SEQ ID NO: 5534
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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ID ABS30826 standard; DNA; 360
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Best Local Similarity 99.0%;
Matches 198; Conservative
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(first entry)
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  05-NOV-2001
                                            Human brain
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed sepecification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTAAGTTA 120
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                                                                                                                    Human, single exon nucleic acid probe, liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
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99.0%; Pred. No. 6.4e-30;
live 0; Mismatches 2;
                                                                                     Human liver single exon probe, SEQ ID No 5816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5816; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
2000US-00608408.
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                                                 (first entry)
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Best Local Similarity 99.0
Matches 198; Conservative
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                  ABS30826;
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AATTGCTTTTCCTCTTGTAC 200

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47 AATTGCTTTTCCTCTTGAAC 28
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Scoring table:

Searched:

Database

Perfect score:

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Sequence:

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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 315 9265
Fax: 319 315 9565
Email: bento-goares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-36, >AT rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                   BU729482
UI-E-CL1-afe-p-03-0-UI.sl UI-E-CL1 Homo sapiens CDNA clone
UI-E-CL1-afe-p-03-0-UI 3', mRNA sequence.
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/tissue type="human retina"
/dev tagage="adult"
/lab host="DHNOB (Life Technologies) (Tl phage resistant)"
/clone lib="UI-E-CL1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 420, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                        ALIGNMENTS
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97044477
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AA047236
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AUTHORS
TITLE
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BM996167 UI H-DH0-
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AUTHORS
TITLE
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modified polylinker; Site_1: ECOR I; Site_2: Not I; UI-E-CLI is a normalized CDNA library confaining the UI-E-CLI is a normalized CDNA library confaining the following tissue(s): retina. The library was constructed following tissue(s): retina and Soares, Genome Research, according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed eight a nolisgo-dT primer containing a Not I site. Double with an olisgo-dT primer containing a Not I site. Double with Not I, and cloned directionally into pT713-Pac with Not I, and cloned directionally into pT713-Pac vector. The oligonacleotide used to prime the synthesis of vector. The oligonacleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The located for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI).

TAG_IISUE-human retina
TAG_LIB-UI-E-CLI
TAG_SEQ-CCGGC"
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1 (bases 1 to 450)

1 (bases 1 to 450)

1 Hiller, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1997)

Contact: Wilson RK
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This clone is available royalty-free through LLNL ; contact the IMAGE clone is available royalty-free through LLNL ; contaction. IMAGE Consortium (infc@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.
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99.2%; Score 198.4; DB 5;
Best Local Similarity 99.5%; Pred. No. 3.8e-31;
Matches 199; Conservative 0; Mismatches 1;
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/mol_type="mRNA"
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AI720016.1 GI:5037272
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Homo saplens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 456)

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Railonal Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contect: Robert Strausberg, Ph.D.

Contect: Robert Strausberg, Ph.D.

Email: Gapbbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Fissue Procurement: Christopher Moskaluk, M.D., Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.

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CO
                                                                            /dev stage="adult, age 25"
/dev stage="adult, age 25"
/lab_host="bH10B (phage resistant)"
/lab_host="bH10B (colon HPIRB)"
/clone_lib="Barstead colon HPIRB7"
/clone="forgan: colon; vector: pT7T3D-Pac (Pharmacia) with a /clone="forgan" colon; vector: pT7T3D-Pac (Pharmacia) with a double-ptylinker; site 1: EcoR1; Site 2: Not1: last modified polylinker; site 1: EcoR1; Site 2: Not1: last modified polylinker; site 1: EcoR1; Site 2: Not1: last modified polylinker; site 3: j. double-stranded cDNA was ligated to Eco RI adaptors 3: j; double-stranded cDNA was ligated to Eco RI adaptors 3: j; double-stranded cDNA was ligated to Eco RI sites of with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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Location/Qualifiers
/db_xref="taxon:9606"
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Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soareseniowa.edu
The following repetitive elements were found in this cDNA
Sequence: 1-36, AAT_rich#Low_complexity (matched compliment)
Seq primer: Mi3 FORWARD
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I (bases 1 to 462).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/clone="IMAGE:2422793"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 198.4; DB 1;
Pred. No. 3.8e-31;
0; Mismatches 1;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 AATTGCTTTTCCTCTTGAAC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA437924.1 GI:24802344
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Best Local Similarity 99.5%;
Matches 199; Conservative (
                                                                                                              metastatic)"
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Homo sapiens
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Unpublished (1997)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 471)

1. (Dases 1 to 71)

1. (Dases 1 to 71)

1. (Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),

1. Unpublished (1997)

1. Contact: Robert Strausberg, Ph.D.

1. Email: cgapbs-r@mail.nih.gov

1. Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

1. Emmert-Buck, M.D., Ph.D.

1. CDNA Library Preparation: M. Bento Soares, Ph.D.

1. CDNA Library Preparation: M. Bento Soares, Ph.D.

1. CDNA Library Arrayed by: Greg Lennon, Ph.D.

1. DNA Sequencing by: Washington University Genome Sequencing Center

1. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AATTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 TIGATGITITAAGITITATCITICATGGTACIAGTGTTTTTTAGATACAGAGACTIGGGGA 185
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                                             /tissue_type="Metastatic Chondrosarcoma"
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Pred. No. 3.8e-31;
clone="UI-H-DH0-aur-1-19-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
99.2%; Score 198.4;
Best Local Similarity 99.5%; Pred. No. 3.8e
Matches 199; Conservative 0; Mismatches
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TAG_LIB=UI-H-DH0
TAG_SEQ=AGATCATTGC"
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FEATURES

ORIGIN

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/organism="Homo Bapleis":

/mol Lype="MRNA"

/db xrefe="taxon:9606"

/clone="IMAGE:3703992"

/tissue_type="carcinoid"

/lab host="DH108"

/clone lib="NCI CGAP LU24"

/note="Torgan: lung; Vector: pT7T3D-pac (Pharmacia) with a /note="Torgan: lung; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized modified polylinker; plasmid DNA from the normalized modified polylinker; plasmid DNA from the normalized modified polylinker; plasmid DNA from the normalized modified to rother was PCR-amplified colNAs from a pol of 5,000 The driver was PCR-amplified colNAs from a pool of 5,000 clones made from the same library (cloneIDs clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mamalia; Eutheria; Drimates; Catarrhini; Hominidae; Homo. Mistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A., Touchman, J.W., Bodifard, G., Smith, D. and Peterson, K. Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD673147 506 bp mRNA linear EST 24-JUN-2003 Eg21d04.yl Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone fg21d04.5', mRNA sequence.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 198.4; DB 2;
99.5%; Pred. No. 3.8e-31;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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Plate: 21 row: d column: 04
Seq primer: M13RP1 reverse primer (ABI).
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22103462
Location/Qualifiers
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Best Local Similarity 99.5
Matches 199; Conservative
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                                                                                                                                            / organis="Homo sapiens"

// organis="Homo sapiens"

// organ="mRNA"

// or xref="taxon:9606"

// clone="IMAGE:1585081"

// lab host="MILOS"

// lab host="MIC GAP Lus"

// lab host="lung Vector: pT/T3D-Pac (Pharmacia) with a /note="Organ: lung; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker: lst strand cDNA was prepared from modified polylinker: lst strand cDNA was prepared from medicied polylinker: lost stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
clone distribution: NOT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Libri, send email to:
hiftoginage.llnl.gov
High quality sequence stop: 416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 bp mRNA linear EST 30-MAR-2001
7q75a08.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3703982 3'
similar to SW:SY02_HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2
PRECURSOR;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 TIGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTTAGATACAGAGACTTGGGGA 169
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%; Score 198.4; DB 1
99.5%; Pred. No. 3.8e-31;
ive 0; Mismatches 1
                      www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 447.
Location/Qualifiers
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Matches 199; Conservative
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BF224310/c
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//issue_type="rolon tumor, RER+"
/lab_host="noll tumor tumor, RER+"
/lab_host="noll 08"
/clone_lib="NCI_CGAP_CO16"
/note="Organ: colon" Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 114484-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BUS80378 601 bp mRNA linear EST 17-SEP-2002
in33b12.x1 Human Fetal Pancreas 1B Homo sapiens cDNA 3' similar to
SW:SY02_HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 PRECURSOR ;, mRNA
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
I (Dasea I to 601)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
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Brodocrine Pancreas Consortium
Harvacd University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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                                                                                                                /organism="Homo sapiens"
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3323256"
  Seq primer: -40UP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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                                                                                                                                                                                                      /Gloue Ille Ille Indian Ille Coun. (ILLE COUL). A count of the library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by Not1. This Not1 digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (COt 500) with 41 mg of Bio-RNA and vector blocking oligonucleorides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center(NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7h90e01.x1 NCI CGAP CO16 Homo Bapiens cDNA clone IMAGE:3323256 3' similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 BPECURSOR;, mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                       /tissue_type="Iris"
/der_dage="Adult"
/db_host="EMDH108"
/clone_lib="Human Iris cDNA (Normalized): fg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Pred. No. 3.8e-31;
0; Mismatches 1;
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/clone="fg21d04"
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Best Local Similarity 99.5%;
Matches 199; Conservative
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AV717017 635 bp mENA linear EST 16-OCT-2000 AV717017 DCB Homo sapiens cDNA clone DCBEXB06 5', mENA sequence. AV717017 GI:10814169
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Bukaryota;

Bukaryota;

Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.

1 (bases 1 to 635)

Max, Y. (au, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,

Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,

Lu, G., Cheng, Z. and Han, Z.

Homo sapiens colones

Unpublished (2000)
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/coll type="mature"
/lab host="BM25.8"
/clone lib="DCB"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Hanan Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanz@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                          1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATAAATG
                                                                                                                                                                                                                                                                                                                                                                                                        .;
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ilarity 99.5%; Pred. No. 3.8e-31;
Conservative 0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBBXB06"
                                                   /organism="Homo sapiens"
Location/Qualifiers
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                                                                                                                                                                                                                        /organism="Homo sapiens"
// organism="MRNA"
// db_xref="taxon:966"
// tissue type="Fetal Pancreas" (4 Pooled Donors, 18 - 20
// tissue type="Fetal Pancreas"
// dev_stage="Fetal Pancreas"
// dev_stage="Fetal Pancreas"
// incte="Vector: pluescript SK(-); Site_1: NotI; Site_2:
// note="Vector: pluescript SK(-); Site_1: NotI; Site_2:
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1 (bases 1 to 634)

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2 (bay, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Kiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z. and Han, Z.

Homo sapiens cDNA DCB clones
Unpublished (2000)
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Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
35.1 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
76.1 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Fax: 186-21-50801922
Fax: 186-21-50801922
Fax: 186-21-50801922
     Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
finious@imgate.wistl.edu)
Seq primar: -40UF from Gibco
High quality sequence stop: 454.
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Matches 199; Conservative 0; Mismatches 1; Indels 0.
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This clone is available at CHGC in Shanghai.
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/ursanism="Homo sapiens"
// mol type="mRNA"
// db_xref="txxxxn:9606"
// clone="UT-E-C10-aee-g-12-0-UI"
// tissue_type="RPE and Choroid"
// dev_stage="adult".
// dab_host="DH10B (Life Technologies) (T1 phage resistant)"
// dab_host="DH10B (Life Technologies) (T1 phage resistant)"
// clone=lib="UT-E-C10"
// note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
// UI-E-C10 is a cDNA library.containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, eight en oligo-dT primer containing an Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                       BM685551 637 bp mRNA linear EST 27-FEB-2002 UI-E-CIO-aae-g-12-0-UI.rl UI-E-CIO Homo sapiens CDNA clone UI-E-CIO-aae-g-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 8250
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515 TIGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTAGATACAGAGACTTGGGGA 574
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
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Pred. No. 3.8e-31;
0; Mismatches 1;
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I bases I to 637)

Xu, X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens CDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Bax: 86-21-508019192
Bmail: hansgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV717339 EST 16-OCT-2
AV177339 DCB Homo sapiens cDNA clone DCBBXC09 5', mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                       515 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTTAGATACAGAGACTTGGGGA
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   Length 635;
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Score 198.4; DB 1;
Pred. No. 3.8e-31;
0; Mismatches 1;
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llarity 99.5%; Pred. No. 3.8e-31;
Conservative 0; Mismatches 1;
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/organism="Homo sapiens"
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Query Match
Best Local Similarity 99.5%;
Matches 199; Conservative
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Homo sapiens
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Matches 199; Conserv
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TAG_SEQ=AAGTGCTTAC"
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184 AATTGCTTTTCCTCTTGAAC 165
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BM996167/c
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/dlone="UJ-CF-ECI-acj-k-08-0-UI"
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/dab_host="DH108 (Life Technologies) (TI phage resistant)"
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/clone_lb="UJ-CF-ECI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
following issue(s) Normal lung from adult and from fetal
following issue(s) Normal lung from adult and from fetal
following issue(s) Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
constructed according to Bonaldo, Lennon and Soares,
denome Research, 6:791-806, 1996, First strand cDNA
genome Research, 6:791-806, 1996, First strand cDNA
synthesis was primed with an oligo-dT primer containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mcrayeuiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. Dr. M. Bento Soares, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLOME Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
The following repetitive elements were found in this cDNA
The following repetitive elements were found in this cDNA
Seq primer: M13 PORWARD
Seq primer: M13 PORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU681561 640 bp mRNA linear EST 07-0CT-2002 UI-CF-ECI-acj-k-08-0-UI.sl UI-CF-ECI Homo sapiens cDNA clone UI-CF-ECI-acj-k-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 121 TTGATGTTTTAAGTTTATGTTTCATGGTACTAGTGTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                                                          AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
                                                                                                                                               224 AAITTIGITIGITIGAIGIGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 283
                        1 (bases 1 to 640) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
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BU681561.1 GI:23531598
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BU681561/c
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
clone Distribution: Clone distribution information can be found
clone Distribution: Clone distribution information can be found
clone Distribution: Clone distribution information can be found
clone Distribution: AAT rich#Low_complexity (matched compliment)
Sequence: 1-37, AAT rich#Low_complexity (matched compliment)
Sequence: 1-37, AAT rich#Low_complexity (matched compliment)
Seducation: M.J. FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642 bp mRNA linear EST 17-JUN-2002
UI-H-DHO-aun-d-15-0-UI.sl WCI CGAP_DHO Homo sapiens cDNA clone
IMAGE:5871710 3', mRNA sequence.
BM996167
Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligomoufsotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the contains the sequence that is located between the Not I site and the contains a library is
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1 (bases 1 to 642)
NCI-CAR http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                 AAGTGCTTAC.
AAGTGCTTAC.
AAG TISSUEANORMAL Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-ECI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TIGATGITITAAGITIATCITITCAIGGIACTAGIGITITITAGAIACAGAGACTIGGGGA 185
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/clone="INAGE:5871710"
/elssue_type="Metastatic Chondrosarcoma"
/dev_stage="Mault"
/lab_host="DH108" (Life Technologies)"
/clone_lib="NCI_CGAP_DH0"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

99.2%; Score 198.4; DB 5; Length
Best Local Similarity 99.5%; Pred. No. 3.8e-31;
Matches 199; Conservative 0; Mismatches 1; Indels
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site_2: Not I; NCI_CGAP_DHO is a cDNA library containing the following tissue(s): vS-8 cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soarce, Genome Research, 6:791-86, 1966, 1966, 1961 strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)lab tail. The sequence tag for this library is AGATCATTGC.

TAG_LIBSUE-H-DHO
TAG_LIB-UI-H-DHO
TAG_SEQ=AGATCATTGC"
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ORIGIN

0; Gaps Query Match 99.2%; Score 198.4; DB 5; Length 642; Best Local Similarity 99.5%; Pred. No. 3.8e-31; Matches 199; Conservative 0; Mismatches 1; Indels 0; ò

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121 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180 304 AATTIGITIGITIGITIGAGAACATTAGGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 245 244 TIGAIGITITIAAGITITATCITICAIGGIACTAGIGITITITIAGATACAGAGACTIGGGGA 185 ద ઠે g

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Search completed: August 4, 2005, 14:32:05 Job time : 951.968 secs

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Sequence 106, App
Sequence 104, App
Sequence 104, App
Sequence 1357, Ap
Sequence 761, App
Sequence 761, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 1362, A
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1344, Ap
Sequence 25, Appl
Sequence 1165, Ap
Patent No. 5212073
Patent No. 5212073
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Sequence 10, Appl
Sequence 10, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 11, Appli
                                                                              August 4, 2005, 07:01:49; Search time 41.2146 Seconds (without alignments) 7940.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          US-09-899-276C-2
200
1 tgcagctaacttattttccc......aattgcttttcctttgtac 200
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                                                                                                                                                                                                                                                                                                                                                                                                                           1: /cgm2 6/ptcdata/1/ina/5A COMB.seq:*
2: /cgm2 6/ptcdata/1/ina/5B_COMB.seq:*
3: /cgm2 6/ptcdata/1/ina/6A_COMB.seq:*
4: /cgm2 6/ptcdata/1/ina/6B_COMB.seq:*
5: /cgm2 6/ptcdata/1/ina/PCTUS COMB.seq:*
6: /cgm2 6/ptcdata/1/ina/PcTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-148-545-106

US-09-148-545-104

US-09-105-434-1033

US-09-902-540-1357

US-09-949-016-13165

US-09-949-016-13165

US-09-949-016-13362

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US-09-77-430C-72
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US-09-023-655-1344
US-07-927-391-25
US-09-023-655-1165
5212073-1
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                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1738
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                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                    Run on:
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No.
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Sequence 16964,

US-10-159-151-1 US-09-949-016-14150 US-09-949-016-182221 US-09-949-016-16964

601 133358

28 39 19:5 133360 4 US-09-949-016-12651 29 38.8 19:4 1203 4 US-09-962-201-201 31 38.8 19:4 124 246 3 US-09-63-706-3 31 38.8 19:4 124 4 2246 4 US-09-863-706-3 31 38.8 19:4 12.2 260293 4 US-09-949-016-125597 33 38.4 19:2 260293 4 US-09-949-016-125597 35 38.4 19:2 260293 4 US-09-949-016-12016 35 38.4 19:2 260293 4 US-09-949-016-12016 36 38.2 19:1 267036 4 US-09-949-016-12016 37 38.2 19:1 26774 4 US-09-949-016-12016 38 18:2 2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 38.2 19:1 2677 4 US-09-949-016-12016 39 39.8 19:0 1051 4 US-09-949-016-12016 39 39.8 19:0 1051 4 US-09-949-016-12016 39 39.8 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 39 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30 19:0 1051 4 US-09-949-016-12016 30	Sequence 12651, A Sequence 1280, Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications of Applications		
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RESULT 3
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yeaquence 72, Application Straypozynaki, Zbigniew
yepticann: Lyanichev, Victor
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ilarity 54.0%; Pred. No. 2.3e-38;
Conservative 90; Mismatches 2;
                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                              1 recagetaacttatttrecectagettrececagacace
                                                                                                                                                                           Query Match 99.2%; Score 198.4; DB 4 Best Local Similarity 99.5%; Pred. No. 9.6e-39; Matches 199; Conservative 0; Mismatches 1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic US-09-777-430C-72
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                        73..369
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US-09-777-430C-72
                                                                          NAME/KEY:
LOCATION:
US-08-437-306-1
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Sequence 3, Application US/09591992
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; Patent No. 655418
; Patent No. 655418
; Patent Nordwarion:
APPLICANT: Gallo, Robert C.
APPLICANT: Devico, Anthony L.
APPLICANT: Garzino, Alfedo
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE REFREENCE: 4115-109 CIP-12
CURRENT APPLICATION NUMBER: US/09/591,992
CURRENT FILING DATE: 1200-06-12
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1997-12-11
; WUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
LENGTH: 725
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COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 196.8; DB 4
Pred. No. 2.3e-38;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: INCYTE PHARMACEUTICALS, INC.
3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-003-655-1344
Sequence 1344, Application US/09023655
Fatent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION FUNDRER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0°
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-591-992-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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455 AATTITGTIGIIGAAACATIAIGCCIIAAGIIAATGIIAAATTCTTAAITTAAGIIA 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1165, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan G. Stuart
APPLICANT: Geffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPEY disk
COMPUTER: PROPEY disk
COMPUTER: PROPEY DE-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 196.8; DB 3;
Pred. No. 2.3e-38;
0; Mismatches 2;
                        FILING DATE: 19920929
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERNCE/DOCKET NUMBER: 16781/369
TELEPHONE: (703) 693-9300
TELEPHONE: (703) 693-9109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AATTGCTTTTCCTCTTGTAC 200
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99.0%;
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 741 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear MOLECTULE TYPE: CDNA US-07-927-391-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.01
Matches 198; Conservative
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APPLICATION NUMBER:
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TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: FOLEY & LARDNER
STREET: Ring Street Station, Suite 500, 1800 Diagonal
STREET: Ring Street Station, Suite 500, 1800 CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AATTTTGTTGTTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTTATTATAATG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 196.8; DB 4;
Pred. No. 2.3e-38;
0; Mismatches 2;
                                                                                               FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Scaller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 94-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-4166
INFORMATION FOR SED ID NO: 1344:
SEQUENATION FOR SED ID NO: 1344:
SEQUENATION FOR SED ID NO: 1344:
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Patent No. 6001649
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: WINTY, Adrian
APPLICANT: VITA, Natalio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AATTGCTTTTCCTCTTGTAC 200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE: HEREWITH
                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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US-09-023-655-1344
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98.4%; Score 196.8; DB 6; Length 752;
Best Local Similarity 99.0%; Pred. No. 2.3e-38;
Matches 198; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                              Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5212073
, Patent No. 5212073
, APPLICANT: ROLLINS, BARRETT; STILES, CHARLES, WONG, GORDON G.
, TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                              1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGT
                                                                                                                                                                                                           Score 196.8; DB 4;
Pred. No. 2.3e-38;
0; Mismatches 2;
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPANTION INFORMATION:
TELEPANTIC (650) 845-0555
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008
FILING DATE:12-MAY-1989
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                                                                                                                                                                                                                                         Conservative
                                                                                                                                                   ; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g187434
US-09-023-655-1165
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 752
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                                                                                                                                                                                                                                                                                                                                                           Length 752;
5212073-1
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT; STILES, CHARLES; WONG, GORDON G.
; APPLICANT: ROLLINS: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; CURRENT APPLICATION DATA:
; CREENT APPLICATION DATA:
; FILING DATE:12-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                           Score 196.8; DB 6;
Pred. No. 2.3e-38;
0; Mismatches 2;
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TITLE OF INVENTION: 70 Human Secreted Proteins
TITLE OF INVENTION: 70 Human Secreted Proteins
TITLE OF INVENTION: 70 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER PELING DATE: 1997-03-07
EARLIER PELING DATE: 1997-03-07
EARLIER PELING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PLING DATE: 1997-03-07
EARLIER PLING DATE: 1997-03-07
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R APPLICATION NUMBER: 60/047,492
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R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-38

R PILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,568

R PILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,314

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R APPLICATION NUMBER: 60/048,974
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,886 APPLICATION NUMBER: 60/047,618 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,503 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 EARLIER APPLICATION NUMBER: 60/056,662 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,617 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 FILING DATE: 1997-08-22 LING DATE: 1997-05-2 BARLIER
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R APPLICATION NUMBER: 60/047,599
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APPLICANT: ROSEN et al.
TITLE OF INVERTION: 70 Human Secreted Proteins
FILLE REFERENCE: P5001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
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Pred. No. 2.6e-38;
0; Mismatches 2;
                  EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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; Sequence 105, Application US/09148545
partent No. 6590075
; GENERAL INFORMATION:
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Best Local Similarity 99.0%;
Matches 198; Conservative
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RE FILING DATE: 1997-04-11

RA APPLICATION NUMBER: 60/043,669

RE FILING DATE: 1997-04-11

RAPPLICATION NUMBER: 60/043,312

RAPLICATION NUMBER: 60/043,313

RE FILING DATE: 1997-04-11

RE FILING DATE: 1997-04-11

RE PLING DATE: 1997-04-11

RE APPLICATION NUMBER: 60/043,672

RE FILING DATE: 1997-04-11

RAPPLICATION NUMBER: 60/048,974

RE FILING DATE: 1997-06-11

RAPPLICATION NUMBER: 60/066,896

RE FILING DATE: 1997-06-05

RE PILING DATE: 1997-06-05

RE PILING DATE: 1997-06-05

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RE RELING DATE: 1997-06-05

RE PILING DATE: 1997-06-05

RE PILING DATE: 1997-06-05

RE PILING DATE: 1997-06-22

RE PLING DATE: 1997-08-22

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RAPPLICATION NUMBER: 60/043,568

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,314

RR FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569
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ER APPLICATION NUMBER: 60/047,500
ER PILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
                                                                                              R APPLICATION DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,617
R APPLICATION NUMBER: 60/047,618
R APLICATION NUMBER: 60/047,618
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,503
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,592
R APPLICATION NUMBER: 60/047,592
R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,583
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R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,879
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/056,910

R PILING DATE: 1997-08-22

R RILING DATE: 1997-08-22

R R PPLING DATE: 1997-08-22

R R PLING DATE: 1997-08-22

R R PLING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,631

R APPLICATION NUMBER: 60/056,845
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R APPLICATION NUMBER: 60/056,892

R FILING DATE: 1997-08-22

R R FILING DATE: 1997-08-23

R R FLING DATE: 1997-05-33

R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/047,599

R APPLICATION NUMBER: 60/047,599

R APPLICATION NUMBER: 60/047,589

R R FILING DATE: 1997-05-33

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                                                                     R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,882

R FILING DATE: 1997-08-22

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R APPLICATION NUMBER: 60/056,903
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R APPLICATION NUMBER: 60/047,614

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,578

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,888
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
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APPLICATION NUMBER: 60/047,593
                   60/056,662
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FILING DATE: 1997-08-22
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                                                       APPLICATION NUMBER: 60/056,872
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               PLICATION NUMBER: 60/
LING DATE: 1997-08-22
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Sequence 104, Application US/09814915A

Batent No. 6750015

GENERAL INFORMATION:
APPLICANT: HOTWItz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods RelaTITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT PILING DATE: 2002-03-21

PRIOR FILING DATE: 2000-06-28 ö 1425 recaectaactratririceceraectriceceaeacaeceretrirarrarraraare 1484 1545 TIGAIGTITTAAGTITATCTITCAIGGTACTAGIGTTTTTTTAGATACAGAGACTIGGGGA 1604 61 AATTITGTITGTIGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120 121 TTGATGTTTTAAGTTTATCTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180 357 IGCTARCTARTITICCCCTAGCTTTCCCCAGACATCCTGTTTTATTATATATG 416 1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCCTTGTTTTATTATAATG 1485 AATTTTGTTGTTGTTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTTATTATTAATG Gapa ö Length 1822; 97.6%; Score 195.2; DB 4; Length 661; 98.5%; Pred. No. 5.5e-38; ive 0; Mismatches 3; Indels 0 2; Indels 98.4%; Score 196.8; DB 4; 99.0%; Pred. No. 2.6e-38; ive 0; Mismatches 2; EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER PEDPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-22
EARLIER PILING DATE: 1997-06-65
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280 1605 AATTGCTTTTCCTCTTGAAC 1624 181 AATTGCTTTTCCTCTTGTAC 200 NUMBER OF SEQ ID NOS: 108 SOFTWARE: Patentin version 3.1 SEQ ID NO 104 Best Local Similarity 99.0 Matches 198; Conservative Query Match Best Local Similarity 98.5 Matches 197; Conservative Homo sapiens US-09-814-915A-104 US-09-814-915A-104 Q ID NO 105 LENGTH: 1822 TYPE: DNA ORGANISM: Query Match 셤 셤 ò a ઠ δ ઠે ઠે

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US-09-328-352-761

j Sequence 761, Application US/09328352

j Sequence 761, Application US/09328352

j Patent No. 6562958

j Patent No. 656298

j GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPBUTICS

TITLE OF INVENTION: UNMBER: US/09/328,352

CURRENT APPLICATION UNMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 761
           Sequence 1357, Application US/09902540

| Sequence 1357, Application US/09902540
| Patent No. 6833447
| GENERAL INPORMATION:
| APPLICANT: Hinkle, Gregory J. APPLICANT: Glater, Steven C. APPLICANT: Wisegand, Roger C. APPLICANT: Wisegand, Roger C. TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof TILE REFERENCE: 38-10(15849) B
| CURRENT APPLICATION NUMBER: US/09/902,540 |
| CURRENT PILING DATE: 2001-07-10 |
| PRIOR APPLICATION NUMBER: 60/217,883 |
| PRIOR FILING DATE: 2000-07-10 |
| NUMBER OF SEQ ID NOS: 16825 |
| SEQ ID NO 1357 |
| LENGTH: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 TGTTAATTCTTAATTTAAGTTATTGATGTTTTAAGTTTTATCTTTCATGGTACTAGTGTTTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 idiihriinairiaaaadairciaaidriaaarricaairiirirriadcaairciaiii 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 דִיִּדִילִידִּלִידִילִידִילִידִילִידִילִידִידִילִידִידִילִידִידִילִידִילִידִילִילִילִילִילִילִילִילִילִילִילִילִי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GITTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTAATTTAAGTTATTGATG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 TTGTTTTATTTTATAAATGAATTTTGTTTGATGTGAAACATTATGCCTTAAGTAA
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Pred. No. 0.14;
0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.8%; Score 43.6; DB 4;
54.8%; Pred. No. 0.11;
iive 0; Mismatches 70;
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LOCATION: (1)..(612)

1 LOCATION: (1)..(612)

1 OTHER INDEMATION: unsure at all n locations

US-09-902-540-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA CONGANISM: Acinetobacter baumannii US-09-328-352-761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.6%;
Best Local Similarity 56.2%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.8°
Best Local Similarity 54.8
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 TCATGG-TACTAGTGTTTTTTAGATACAGAGACTTGGGGAAATTGCTTTTCCTCTTGT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TIGATGITITAAGITITATCITICATGGTACTAGTGTTTTTTAGATACAGAGTTGGGGA 180
                     Gaps
AATTTGTTGTTGATGTGAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
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                                                                                                                                                                                                                                                                                                                Sequence 1033, Application US/09016434
Sequence 1033, Application US/09016434
Patent No. 650091
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.6%; Score 45.2; DB 4; Length 840; 66.9%; Pred. No. 0.049; 11ve 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: BM PC compatible COMPUTER: BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS GURERY APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION: APPLICATION: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:

RIGHOR DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELEPANE. (650) 845-0555

TELEPHANE: (650) 845-0555

TELEPHANE: (650) 845-1166

INFORMATION FOR SEQ ID NO: 1033:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: INCYTE PHARMACEUTICALS, INC. 3174 PORTER DRIVE
                                                                                                                                                                             181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                                         537 AATTGCTTTTCCTCTTGAAC 556
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Best Local Similarity 66.9
Matches 79; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAN-
TOPOLOGY: Linea-
IMMEDIATE SOURCE:
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CLONE: 965517
US-09-016-434-1033
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Sequence 13165, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; PAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TILE REPERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PAPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-0-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOPTHARE: FEBSICS for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 TGCCTTAAGTAATGTTAATTCTTAATTTAAGTTATTGATGTTTTAAGTTTATCTTTCATGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.6%; Score 43.2; DB 4; Length 346112; Best Local Similarity 56.2%; Pred. No. 0.36; Matches 81; Conservative 0; Mismatches 63; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167908 TTGCCTGGGTTTTAAGTATTTGAG 167931
160 TTAGATACAGAGACTTGGGGAAAT 183
                                             440 TTACTTTAGGATGTATAGTTCAAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TACTAGTGTTTTTAGATACAGAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(346112)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                     US-09-949-016-13165
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LENGTH: 346112
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Search completed: August 4, 2005, 14:40:35 Job time : 43.2146 Becs

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August 4, 2005, 08:04:16; Search time 356.761 Seconds (without alignments) 3633.986 Million cell updates/sec
                                                                                          US-09-899-276C-2
200
1 tgcagctaacttattttccc.....aattgcttttcctcttgtac 200
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                            7297361 segs, 3241162794 residues
                                                                                                                                                                                                                                                                     Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                               Sequence:
                                                                                                                                                            Searched:
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                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score March Length DB ID  1 200 100.0 200 9 US-09-899-276-2 2 198.4 99.2 489 10 US-09-918-995-6347 5 198.4 99.2 1472 16 US-10-133-013-211 5 198.4 99.2 1472 16 US-10-133-013-211 5 198.4 99.2 11793 19 US-10-247-671-41 5 198.8 98.4 360 9 US-08-94-948 5 198.8 98.4 360 10 US-10-685-705-4 5 196.8 98.4 508 19 US-10-775-169-294 5 Sequence 5454, Appli			•			SUMMARIES		
Score Match Length DB ID  200 100.0 200 9 US-09-899-276-2 198.4 99.2 489 10 US-09-918-95-6347 198.4 99.2 1472 16 US-10-133-013-211 198.4 99.2 11793 19 US-10-247-671-41 196.8 98.4 360 9 US-09-864-761-5454 196.8 98.4 508 19 US-10-775-169-294	sult		* Ouerv					
100.0 200 9 US-09-899-276-2 99.2 489 10 US-09-918-995-6347 99.2 1005 16 US-10-133-013-211 99.2 11793 19 US-10-847-671-41 98.4 360 9 US-09-864-761-5454 98.4 508 19 US-10-775-169-294	No.	Score	Match	Length	DB	ID	Description	
99.2 489 10 US-09-918-995-6347 99.2 1005 16 US-10-133-013-211 99.2 1472 16 US-10-247-671-41 99.2 11793 19 US-10-685-705-4 98.4 508 19 US-10-775-169-294		200		!	6	US-09-899-276-2	Sequence 2. Appli	
99.2 1005 16 US-10-133-013-211 99.2 1472 16 US-10-247-671-41 99.2 11793 19 US-10-685-705-4 98.4 360 9 US-09-864-761-5454 98.4 508 19 US-10-775-169-294	7	198.4			10	US-09-918-995-6347	Sequence 6347, Ap	
99.2 1472 16 US-10-247-671-41 99.2 11793 19 US-10-685-705-4 98.4 360 9 US-09-864-761-5454 98.4 508 19 US-10-775-169-294	m	198.4	99.2		16	US-10-133-013-211	Sequence 211, App	
99.2 11793 19 US-10-685-705-4 98.4 360 9 US-09-864-761-5454 98.4 508 19 US-10-775-169-294	4	198.4	99.5		16	US-10-247-671-41	Sequence 41, Appl	
98.4 360 9 US-09-864-761-5454 98.4 508 19 US-10-775-169-294	Ŋ	198.4	99.5	_	13	US-10-685-705-4	Sequence 4, Appli	
98.4 508 19 US-10-775-169-294	9	196.8	98.4		σ	US-09-864-761-5454	Sequence 5454, Ap	
	7	196.8	98.4		19	US-10-775-169-294	Sequence 294, App	

72, 74, 72, 74, 74, 74, 74, 74, 74, 74, 74, 74, 74	Sequence 411, Appl Sequence 41, Appl Sequence 106, App Sequence 106, App Sequence 105, App Sequence 105, App Sequence 8779, Ap Sequence 8779, Ap Sequence 8779, Ap
9 US-09-777-430A-72 22 US-10-875-094-72 18 US-10-210-120-66 19 US-10-210-120-66 19 US-10-263-975A-58 19 US-10-263-975A-58 19 US-10-263-975A-58 19 US-10-852-335A-46 21 US-10-852-335A-46 22 US-10-852-335A-46 23 US-10-852-335A-46 24 US-10-909-035-66 25 US-10-305-66 26 US-10-306-35A-36 27 US-10-306-36 28 US-10-342-887-849 28 US-10-342-887-849 29 US-10-278-698-35 21 US-10-278-698-35 21 US-10-278-698-35 21 US-10-342-887-849 22 US-10-342-887-849 23 US-10-685-705-1 24 US-10-685-705-1 25 US-10-398-36-37 26 US-10-398-36-37 27 US-10-388-36-37 28 US-10-685-705-1 29 US-10-685-705-1 20 US-10-388-360-377 20 US-10-388-360-377 20 US-10-38-360-373-37	5 5 5
66 444777777777777777777777777777777777	11000 11000 1001 1001 1001 1000 1000 1
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	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

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APPLICANT: 2UT Hausen, Harald
APPLICANT: 2UT Hausen, Harald
APPLICANT: 2UT Hausen, Harald
APPLICANT: Patzelt, Andrea
TITLE OF INVENTION: No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
FILE REFERENCE: 012627-023
CURRENT FILING DATE: 2001-07-06
CURRENT FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 200; DB 9; Length 200; 100.0%; Pred. No. 2e-32; ive 0; Mismatches 0; Indels
                      Sequence 2, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
                                                                                                    APPLICANT: Rosl, Frank
APPLICANT: Soto, Ubaldo
APPLICANT:
Coy, Johannes
APPLICANT: Finzer, Patrick
APPLICANT: Pelius, Hajo
APPLICANT: Pouska, Annemarie
APPLICANT: zur Hausen, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
, ORGANISM: Homo sapiens
US-09-899-276-2
US-09-899-276-2
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Query Match
Best Local Similarity 99.5
Matches 199; Conservative
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ORGANISM: Homo sapiens
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US-10-247-671-41/c
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                                                                                                        TIGATGITITAAGITITATCITICATGGTACTAGIGTTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                           AATTITGITTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
                                                           Gaps
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ilarity 99.5%; Pred. No. 5.4e-32;
Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                  Sequence 6447, Application US/09918995

publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLING DATE: 2001-07-30
PRIOR FILLING DATE: 2001-07-30
SPIOR FILLING DATE: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Astromoff, Anna
APPLICANT: Astromoff, Anna
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-133-013-211/c
Sequence 211, Application US/10133013
Sequence 211, Application US/1013013
Sequence 211, Application US/10130130166903A1
GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (1)...(489)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-6347
                                                                                                                                                                                181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 199; Conservat
                                                                                                                                                                                                                                                                                     US-09-918-995-6347
                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ȚIGAIGITITAAGITITATCITICAIGGIACIAGIGITITITAGALACAGAGAGAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                            228
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; Sequence 41, Application US/10247671
; Publication Wo. US20030194721A1
; Publication Wo. US20030194721A1
; GENERAL INFORMATION:
    APPLICANT: Mikita, Thomas
    APPLICANT: Mikita, Thomas
    APPLICANT: Mikita, Thomas
    APPLICANT: Mikita, Thomas
    APPLICANT: Maser, Matthew R.
    APPLICANT: Kaser, Matthew R.
    APPLICANT: Kaser, Matthew R.
    APPLICANT: Kaser, Matthew R.
    APPLICANT: Maser, Matthew R.
    APPLICANT: WINGER: 2002-09-18
    CURRENT FILING DATE: 2002-09-18
    PRIOR FILING DATE: 2001-09-19
    NUMBER: PERL PROGRAM
    SEQ ID NOS: 186
    SOFTWARE: PERL PROGRAM
    SEQ ID NO 41
    LENDY HAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

'NAME/KEY: misc_feature

'OTHER INFORMATION: Incyte ID No. US20030194721A1 989010.6

US-10-247-671-41
                                                                                                                                                                                                                                                                                                                Query Match 99.2%; Score 198.4; DB 16; Length Best Local Similarity 99.5%; Pred. No. 6.6e-32; Matches 199; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                    FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SCPTWARE: PERL PROGRAM
SEQ ID NO 211
LENGTH: 1005
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AATTGCTTTTCCTCTTGTAC 200
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61 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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Pred. No. 1.1e-31;
0; Mismatches 2; Indels 0
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN PULCENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 3.7
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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US-10-775-169-294
; Sequence 294, Application US/10775169
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Matches 198; Conservative
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ORGANISM: Homo sapiens
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Sequence 5454, Application US/09864761

Fatent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: US000-05-26

PRIOR PILING DATE: US000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10685705

Publication No. US20040177387A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: University of Kentucky Research Foundation

APPLICANT: JAXAKRISHNA, Ambati

TITLE OF INVENTION: Defeneration

FILE REFERENCE: 050229-0415

CURRENT APPLICATION NUMBER: US/10/685,705

CURRENT APPLICATION NUMBER: 60422,096

PRIOR APPLICATION NUMBER: 60422,096

PRIOR FILING DATE: 2002-10-30
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      287 AATTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 228
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Pred. No. 1.3e-31;
0; Mismatches 1;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 11793
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Best Local Similarity 99.5%;
Matches 199; Conservative
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US-10-875-094-72
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Sequence 72, Application US/10875094
Sequence 72, Application US/10875094
Sequence 72, Application Wo. US20050130179A1
SUBJICATION: US. USZ0050130179A1
SPELICANT: Ilyamichev, Victor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Mayland, Sarah R.
APPLICANT: Takova, Tsetska
APPLICANT: Prudent, James R.
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
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98.4%; Score 196.8; DB 22; Length 647;
Best Local Similarity 54.0%; Pred. No. 1.3e-31;
Matches 108; Conservative 90; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AATTGCTTTTCCTTGTAC 200
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US-09-77-430A-72
Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Sequence 72, Application Sequence 72
APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Allawi, Hatim T.
APPLICANT: Allawi, Hatim T.
APPLICANT: Takevar, Teeteska
APPLICANT: Takevar, Teeteska
APPLICANT: Post-oe P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REPERBRÜCE: POSS-04912
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 72
LIENGTH 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (33).-(199)
OTHER INFORMATION: Bach "n" represents a nucleotide selected from a, t, g or c,
OTHER INFORMATION: contains no nucleotide.
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                              APPLICANT: Burczynski, Michael
APPLICANT: Thie, Matalie
APPLICANT: Transe, Matalie
APPLICANT: Trepicchio, Milliam
APPLICANT: Trepicchio, Milliam
APPLICANT: Trepicchio, Milliam
APPLICANT: Trepicchio, Milliam
TITUE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (331896-01300)
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: Patentin Version 3.2
SEQ ID NO 294
LENGTH: 508
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98.4%; Score 196.8; DB 19; Length 508;
Best Local Similarity 99.0%; Pred. No. 1.2e-31;
Matches 198; Conservative 0; Mismatches 2; Indels 0;
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98.4%; Score 196.8; DB 9;
Best Local Similarity 54.0%; Pred. No. 1.3e-31;
Matches 108; Conservative 90; Mismatches 2;
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ORGANISM: Artificial Sequence
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                   Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-10-775-169-294
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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181 AATTGCTTTTCCTCTTGTAC 200
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                                           SEQUENCE CHARACTERISTICS:
LENGTH: 725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
          TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO: 1344:
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Best Local Similarity 99.0%;
Matches 198; Conservative
                                                                                                                                                                   LIBRARY: GENBANK
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Matches 198; Conservative
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Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                           Score 196.8; DB 16; Length 725;
Pred. No. 1.3e-31;
0; Mismatches 2; Indels 0;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATE:
FILING DATE: 14-Aug-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTAT
TITLE OF INVESTIGATION: Expression Profile of Prostate Cancer CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT APPLICATION NUMBER: US/0.100,120
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ 1D NOS: 123
SOFTWARE: Patent In version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AATTGCTTTTCCTCTTGTAC 200
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-210-120-66
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                                                                                                                                                                                                     SEQ ID NO 66
LENGTH: 725
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61 AATTTTGTTGTTGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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Publication No. US20040110792A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods For Assessing and Treating Leukemia

FILE REPRENCE: CDS 293 PCT

CURRENT FILING DATE: 2002-10-30

FRIOR APPLICATION NUMBER: 60/340,938

PRIOR APPLICATION NUMBER: 60/340,938

PRIOR APPLICATION NUMBER: 60/340,938

PRIOR APPLICATION NUMBER: 60/340,081

PRIOR APPLICATION NUMBER: 60/340,081

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 900

SOFTWARE: Patentin Version 3.1
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                                                                                                                                          Length 725;
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                                                                                                                                       Score 196.8; DB 18; Length
Pred. No. 1.3e-31;
0; Mismatches 2; Indels
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Pred. No. 1.3e-31;
0; Mismatches 2; Indels
; CLONE: 934513
; SEQUENCE DESCRIPTION: SEQ ID NO: 1344
US-10-641-643-1344
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DB 19;
                                                                                                                                                                                                                             Score 196.8; DB 19;
Pred. No. 1.3e-31;
0; Mismatches 2;
PRIOR FILING DATE: 2000-03-02
PRIOR PEDLICATION NUMBER: US 60/069,281
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AATTGCTTTTCCTCTTGTAC 200
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Best Local Similarity 99.0
Matches 198; Conservative
                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.0
Matches 198; Conservative
                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-445-790-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-335A-46
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APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Barnes, Glenn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
TITLE OF INVENTION: METABOLIC DISORDERS
FILLE REFERENCE: MPI2003-025PIRNM
CURRENT APPLICATION NUMBER: U5/10/764,649
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: 60/446041
PRIOR APPLICATION NUMBER: 60/446041
PRIOR APPLICATION NUMBER: 60/446041
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 725
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Sequence 3, Application US/10445790

Publication No. US20040197305A1

GENERAL INFORMATION:

APPLICANT: DeVico, Anthony L.

APPLICANT: Devico, Anthony L.

TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE REFERENCE: 4115-109 CIP DIV

CURRENT EPLICATION NUMBER: 2003-05-27

PRIOR APPLICATION NUMBER: ECT/US98/26291

PRIOR APPLICATION NUMBER: US 09/591,992

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: U000-12-06

PRIOR PLILNG DATE: U000-12-06

PRIOR PLILNG DATE: U000-12-06
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                           AATTITGTITGTIGATGIGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 498
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      TIGATGTITIAAGTITATCTITCATGGTACTAGTGTTTTTTAGATACAGAGACTIGGGGA 180
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Pred. No. 1.3e-31;
0; Mismatches 2;
                                                                                                                                                                                                                         Sequence 17, Application US/10764649
Publication No. US20040157253A1
GENERAL INFORMATION:
                                                                                   181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                           AATTGCTTTTCCTCTTGAAC 578
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Best Local Similarity 99.0%;
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; LOCATION: (54)...(353)
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ORGANISM: human
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Search completed: August 4, 2005, 15:54:12 Job time : 358.761 secs

us-09-899-276c-2.rnpb

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AY046055 Homo sapi
AC009488 Homo sapi
AC141828 Apis mell
AC089597 Homo sapi
AC08990 Homo sapi
AC17556 Mus muscu
AC17556 Mus muscu
AC132816 Homo sapi
AC117556 Continuation (3 of
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Continuation (4 of
AC17092 Pan trogl
                                                                                                                   AL928956 Mouse DNA
BX537347 Zehref
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 Oryza sat
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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AP004649 C
AC104383 H
AC145968 E
AB100086 I
AC174214 H
AC132561 H
AC027220 H
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Best Local Similarity 100.0%; Pred. No. 3.1e-31;
Matches 150; Conservative 0; Mismatches 0; Indels
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ACCESSION
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Source
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AC093924 Genomic 8
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BT003528 Drosophil
AC147691 Pongo pyg
AC132388 Mus muscu
AC093360 Mus muscu
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AC01520 Homo sapi
AC005549 Homo sapi
M37719 Human monoc
X60001 H sapiens g
AX346555 Sequence
AX346555 Sequence
L32659 Bovine mono
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(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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		COMMENT TO cite this work please use: SeattleSNPs. NHLBI HL66682 Program TO cite this work please use: Seattle, WA (URL: for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu). FEATURES Location/Qualifiers	source 1.317# /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		v	Valiation / requency="0.15" /replace="t" 334		variation   frequency="0.16"   /replace="t"		repeat_region 614. 720 /rpt_family="MIR" /rpt_type=dispersed				variation 1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072   1072	variation 1280 /frequency="0.23" /replace="a" 1537	i~~~	/\r	/requency="0.02"  variation   1707

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                                                                                                                                                                                                                     Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Rosl, F.
Differential transcriptional regulation of the monocyte-chemoatractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin structure and AP-1 composition
00ncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
Heidelberg, FRG
                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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join(<7550. .7685,8468. .8585,8968. .>9073)

1950. .7685

gene="MCP-1"

gene="MCP-1"
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                                                    linear
                                                                                                                      MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
Homo sapiens
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Y18933
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All repeats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

Altrepeats were identified using RepeatMasker.

Altrepeats were identified using RepeatMasker.

Center: Whitehead Institute/ MIT Center for Genome Research
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1 (bases 1 to 73806)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-329H16

Unpublished
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                                                   1 CAAAGATCACATTCTAGGTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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Homo sapiens chromosome 17 clone RP11-329H16 map 17, LOW-PASS
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Length 73806;

98.9%; Score 148.4; DB 2;

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Direct Submated (127-AUG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 147416)

Sa Sharen, B., Fasman,K., Linton,L., Nusbaum,C., Lander,B., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Boutwell,C., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collymore,A., Cooke,P., Corliss,D., Depayre,B., Devon,K., Dewar,K., Donelan,L., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gardyna,S., Geraigery,K., Grant,G., Hagos,B., Heaford,A., Herena,L., Horton,L., Howland,J.C., Jones,C., Kann,L., Kartas,A., McGurk,A., McKernan,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., Marquis,N., Morris,W., MocTow,J., Mychaleckyj,J., Nahf,R., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella-Miller,I., Vasailiev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D., Ve,W.J., Zhao,J. and Zody,M.

Direct Submission

AL Subramanian,A. Morsels Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                      ACO05549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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st Local Similarity 99.3%; Pred. No. 2.6e-31; ches 149; Conservative 0; Mismatches 1; Indels
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Homo sapiens chromosome 17, clone hRPK.215_E_13
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complement (3593)
/rpt family="LipA2"
39362. .39414 46184. .46296 /rpt family="MIR" complement (47075. .47140) /rpt family="MLTIG" / LD family (47363. 47442) /rpt family="MLT1G" complement (48165. 48209) family="MLT1J" .41460 complement (47266 . .47307) /rpt\_family="(CA)n" rpt\_family="A-rich" complement (39920. .40047) rpt\_family="MIR" /rpt\_family="MIR" complement(16483, .16653) /rpt\_family="MIR" 16830. .16949 .27950)family="AluJb" /rpt\_family="MER5A" complement(11031. .11072) /rpt\_family="MIR" 11567. .11836 /rpt family="AT\_rich" 24513. 25245 /rpt family="HERVL" 25613. 25758 /rpt\_family="MLT1" 23364. 32581 /rpt\_family="MLT1" /rpt\_family="MLR" /rpt\_family="MLR" family="AT\_rich" rpt\_family="MEK94" 8930. .28968 rpt\_family="AT\_rich" 9960. .30341 20613, .25758 /rpt\_family="HERVL" 26135, .26000 /rpt\_family="LTR16A" 17393. .18306 /rpt\_family="HERVL" 18315. .24307 /rpt\_family="L1PA2" 24309. .24335 rpt family="LTR16A" omplement(27814. .2 /rpt\_family="LTR24" |4781. .44811 . .41469 family="L1PA6" family="MER5A" rpt family="MER5A" 7203. 17380 rpt\_family="LTR16A" family="MER94" /rpt\_family="MER9" complement(12983. rpt family="L2" 2501. .12981 rpt\_family="M 3554. .43983

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Schwarz, E., Fan, E., Kallin, B., Sorrentino, V. and Bloom, B. The IFN-gamma inducible cDNA gamma. 1 is an incompletely spliced JE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-MAY-1991) E. Schwarz, Albert Einstein College of
Medicine, Dept of Microbiology & Immunology, Forchheimer Bldg Room
411, 1300 Morris Park Avenue, Bronx NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                 1304 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                  CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
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H. Bapiens gene for JE protein, exons 3 and 4.
X60001
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     1975. .>2080
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Pred. No. 1.2e-27;
0; Mismatches 1;
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JE protein; secretory protein.
Homo sapiens (human)
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613. .730
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Best Local Similarity 98.7%;
Matches 148; Conservative
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2 (bases 1 to 2243)
Schwarz, E.
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| db_xref="Gis 487124"
| translation="MKVSAALCLLLIAATFIPQGIAQPDAINAPVTCCYNFTNRKIS
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                                                                                                                                                                                                                                                                                                          HUMMCHEMP 2776 bp DNA linear PRI 13-MAY-1994 Human monocyte chemotactic protein gene, complete cds. M37719
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                                                                1 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
                                   0; Gaps
 Score 148.4; DB 9; Length 147416;
Pred. No. 2.3e-31;
0; Mismatches 1; Indels 0; (
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/75. .2080
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Location/Qualifiers
1. 2776
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| /db_xref="taxon:9606"
| /gene="850A2"
| join(598. .673,1472. .1589,1975. .2080)
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monocyte chemotactic protein.
Homo sapiens (human)
Homo sapiens
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/gene="SCYA2"
Query Match
Best Local Similarity 99.3%;
Matches 149; Conservative
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CTCTTCTCCTGCCTGCCTTTTCCTCTTTCTCATGACTCTTTCTGCTCTTAAGATCAGA 120
                                                 CAAAGATCACATTCTAAGCTCTGAAGGTATAGAGAAAGCACTGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                   Location/Qualifiers

1. :5926
| organism="synthetic construct" | /mol_type="unassigned DNA" | /db xref="taxon:32630" | /noTe="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1626 03-JAN-2002;
Epigenomics AG (DE)
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Pred. No. 8.1e-21;
0; Mismatches 24;
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synthetic construct
other sequences; artificial sequences.
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Best Local Similarity 84.0%;
Matches 126; Conservative
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synthetic construct
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3405 bp DNA linear MAM 17-JAN-1995
Bovine monocyte chemoattractant protein-1 (MCP-1) gene exons 1-3,
complete cds.
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Wempe,F., Kuhlmann,J.K. and Scheit,K.H.
Characterization of the bovine monocyte chemoattractant protein-1
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                      Score 92; DB 6; Length 592
Pred. No. 2.4e-15;
0; Mismatches 35; Indels
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Location/Qualifiers
1. .3405
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monocyte chemoattractant protein-1.
Bos taurus (cow)
Bos taurus
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Best Local Similarity 76.4%;
Matches 113; Conservative
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McCombie, W.R.
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Submitted (11-SEP-2001) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
3 (bases 1 to 109929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROD 29-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 TCCTGCCTGCCTTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCA----GAAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (bases 1 to 109929)
MCCombie,W.R., de la Bastide,M., Spiegel,L., Preston,R.,
Kirchoff,K., Kuit,K., Mascimento,L., Zutavern,T., Balija,V.,
Bell,M., Baker,J., Miller,B., Katzenberger,F., Muller,S., King,L.,
                                                                                                                                                                                                                                                                                                                                                                   99
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Genomic sequence for Mus musculus, clone RP23-155E23, from
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                                                                                                                                                                                                                                          Length 3405;
                                                                                                                                                                                                                                    Query Match 39.7%; Score 59.6; DB 4; Best Local Similarity 67.6%; Pred. No. 3e-06; Matches 100; Conservative 0; Mismatches 44;
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AC093922.5 GI:21629259
                      2695. .3227
/gene="MCP-1"
/number=3
3202. .3207
/gene="MCP-1"
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Submitted (16-JUL-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
Harbor, NY 11724, USA
On Jul 26, 2002 this sequence version replaced gi:16117547.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1-e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

RP23-239M9 overlaps clone RP23-155E23 (AC093922) from base 1 to base 56914. The overlap is from base 53016 to base 109929 on
                                                                                                        90164 GAGGGAGAGGGAGAGGGAGGGAGTTATTGATCTTTTTCCTTGGACCCATCCAGCTATT 90105
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Submitted (11-SEP-2001) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
3 (bases 1 to 166277)
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McCombie, W.R., Spiegel, L., de la Bastide, M., Preston, R., Nascimento, L., Zutavern, T., Balija, V., Bell, M., Miller, B., Katzenberger, F., Muller, S., Sullivan, P., Yang, C., Dike, S., Palmer, L., O'Shaughnessy, A. and Dedhia, N. Genomic sequence for Mus musculus, clone RP23-239M9, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
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Genomic sequence for Mus musculus,
Chromsome 17, complete sequence.
/mol_type="genomic DNA/db_xref="taxon:10090"
                                                                                         /clone="RP23-155E23"
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Mus musculus
                                                              chromosome="17"
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McCombie, W.R.
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Best Local Similarity 60.23
Matches 62; Conservative
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On Mar 11, 2003 this sequence version replaced gi:23306132.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequenced with an alternate of hemistry or covered by high quality data (i.e., phred quality chemistry or covered by high quality data (i.e., phred quality as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by more than one plasmid subclone; and the assembly was confirmed by more than one plasmid subclone; and the assembly was confirmed by more than one plasmid subclone; and the assembly was confirmed by senerated by combining Syngenta, Monsanto and Arizona Genomics generated by combining data. There is only Syngenta reads from base 123135-123143 there is an A run where the Syngenta reads express 10 A's and the AGI reads say 9.

There is a run of about 15 C's from base 132783-133796 that has an There is a run of about 15 C's from base 13951-13618 there are Papeats. There are Bacterial Transposons at the 21-30 TA tandem repeats. There are Bacterial Transposons at the
                                                                                                                                                                                                                                                                                                                                                                                                                          AC134230 159270 bp DNA linear PLN 11-MAR-2003 Oryza sativa (japonica cultivar-group) chromosome 3 clone OSJNBA0005J15, complete sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Fracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryzaea;
I (bases 1 to 159270)
I (bases 1 to 159270)
Oryzaea, Vu, Y., Soderlund, C., Kim, H.-R., Rambo, I., Currie, J. and
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Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C.,
Currie, J. and Collura, K.
Direct Submission
Submitted (24-SBE-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                              Gaps
                                                                                                                                                                                                                                                                                                        ch 24.9%; Score 37.4; DB 10; Length 166277; 1 Similarity 60.2%; Pred. No. 2.3; 62; Conservative 0; Mismatches 41; Indels 0; 6
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154360 CTTGCALTAAADAAAAAAGAACGGTTTCTGCAATTTACTTCAGTCTTTTCTTCAAATGCC 154301
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Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jun 13, 2003 this sequence version replaced gi:13359358.
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Homo sapiens genomic DNA, chromosome 11 clone:RP11-748H22, complete
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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2. (bases 1 to 191270)
Hattori, M., Yada, T., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .159270
| Organism="Oryza sativa (japonica cultivar-group)" | Amol type="denomic DNA" | Amol type="denomic DNA" | Amol type="taxon:39947" | Chromosome="3" | Chromosome="3" | Clone="0SJNBa0005J15"
following locations: 78322-81796, 80866-84661, 66433-70443, 65711-69368, 50113-55386, 25635-28807 and 35843-39327. The assembly overlaps from base 157727-159271with OSJNBa0042L15 (accession #AC119748). The overlap is from bases 1-1545 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

24.3$; Score 36.4; DB 9; Length 191270;
Best Local Similarity 54.5$; Pred. No. 4.3;
Matches 73; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.4%; Score 36.6; DB 8; Length 159270; 60.6%; Pred. No. 3.9; 19, 11dels 0; Mismatches 39; Indels 0;
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| /mol_type="genomic DNA"
| /db xref="taxon:9606"
| /chromosome="11"
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Best Local Similarity 60.69
Warches 60; Conservative
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contig of 4568 bp in length
gap of unknown length
contig of 4613 bp in length
contig of 1101 bp in length
contig of 1101 bp in length
gap of unknown length
contig of 20985 bp in length
gap of unknown length
contig of 4757 bp in length
contig of 4757 bp in length
contig of 17540 bp in length
gap of unknown length
contig of 6771 bp in length
gap of unknown length
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/clone_lib="RPCI mouse BAC library 23"
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/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Job time : 608.915 secs
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154300 ACCTAGCATCTTTCTCAGGGCTCTTTTGTGAATATAATATCAATGTAATAGATTTT 154241
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Consensus quality: 192296 bases at least Q30
Consensus quality: 194577 bases at least Q30
Consensus quality: 194577 bases at least Q30
Consensus quality: 194577 bases at least Q30
Estimated insert size: 194000; agarcose-fp estimation
Bstimated insert size: 197111; sum-of-contigs estimation
Quality coverage: 6.22 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.12 in Q20 bases; sum-of-contigs estimation

**NOTE: This is a "working draft" sequence. It currently
**Consists of 24 contigs. Gaps between the contigs

**are represented as runs of N. The contigs

**are represented as runs of N. The contigs

**provided by the submittor.

**This sequence will be replaced

**provided by the submittor.

**This sequence will be preserved.

**This sequence as soon as it is available and

**the accession number will be preserved.

**19139 19238: gap of unknown length

**28744 30952: contig of 1918 bp in length

**28748 : contig of 2109 bp in length

**28749 52508: gap of unknown length

**52409 52508: gap of unknown length

**53106 5745: gap of unknown length

**57316 5745: gap of unknown length

**57316 5745: gap of unknown length

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**77225 contig of 14810 bp in length

**77225 contig of 14810 bp in length

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Mus musculus clone RP23-336A14, WORKING DRAFT SEQUENCE, 24 ordered
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DoE Joint Genome Institute.

Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:8810373.

Center: Joint Genome Institute

Center: Joint Genome Institute
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f unknown length
g of 4999 bp in length
f unknown length
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of 8322 bp in length
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Center Project Name: 1865910
Center clone name: RPCI-23_336A14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC073756.2 GI:9256783
HTG: HTGS PHASE2; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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COMMENT

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156512 AGAAGCAGGGTGATCCCTTGAGCCACTTTTCAGCAACAGGCTGTTTCCTTGTGACATCCC 156453
                                                                                          Gaps
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  Length 198211;
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                                             46; Indels
Query Match 24.3%; Score 36.4; DB 2; Best Local Similarity 58.2%; Pred. No. 4.2; Matches 64; Conservative 0; Mismatches 46;
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August 3, 2005, 15:09:47; Search time 99.413 Seconds (without alignments) 8932.047 Million cell updates/sec
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## ALIGNMENTS

ADH13940 standard; DNA; 150 BP.

RESULT 1

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:3. Poustka A; Delius H, Disclosure; SEQ ID NO 3; 30pp; English. Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. EP1170372-A1. Homo sapiens. 09-JAN-2002. ADH13940; ADH13940
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identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to protein in a sample or purify a natural or the protein from a sample. The nucleotides may be useful for accombinant protein from a sample. The nucleotides may be useful for recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion circulary, restenosis, or stroke. The cDNAs can also be used for large-scale injury, restenosis, or stroke. The cDNAs can also be used for large-scale injury, restenosis, or stroke. The cDNAs can also be used for large-scale concerts or gene expression analysis of several new nucleic acid genetic or gene expression analysis of several new nucleic acid concerts. Antibodies to the proteins encoded by the cDNAs are useful for molecules. Antibodies to the proteins encoded by the cDNAs are useful for associated with abnormalities in the expression, amount or distribution confirmed protein. The present sequence represents a cDNA of the invention confirmed that is differentially expressed in activated vascular tissue. Note: The confirmed and in electronic format directly from USPTO at the present sequence deat and the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the confirmed the conf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 724 BP; 184 A; 180 C; 154 G; 204 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasctropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
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                             pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA #839 differentially expressed in activated vascular tissue.
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                                                                                                                                                                                     Score 150, DB 6;
Pred. No. 2.9e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-0222469P.
08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX63839 standard; cDNA; 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                     Local Similarity 100.
Les 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-110597/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAND/) BANDMAN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002137081-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bandman O;
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                                                                                                                                                                                                     Query Match
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comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN) s comprising two or more of the isolated (PN) s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. ACF64025 to ACF6424 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 STCTTCTCCTGCCTGTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2 ) gene, useful for studying the function of SCYA2 , and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, small inducible cytokine A2; SCYA2; gene; ds; haplotype pair; haplotyping; atherosclerosis; antiarteriosclerotic; gene therapy; single nucleotide polymorphism; genotyping; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                              sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                         Score 149.6; DB 8; Length 750;
Pred. No. 5.8e-34;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                              Sequence 750 BP; 186 A; 199 C; 144 G; 219 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human small inducible cytokine A2 (SCYA2) genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 ATAATCCAGTTCATCCTAAAATGCTTTTTC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATAATCCAGTTCATCCTAAAATGCTTTTTC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
598. .2080
/*tag= a
/product= "Human SCYA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK47979 standard; DNA; 2775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001WO-US026899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2000; 2000US-0228496P.
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.3%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anastasio AE, Finkel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 17q11.2-q21.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-339655/37.
P-PSDB; AAU77179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK47979;
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ABK47979
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                                                                                       This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, Ccr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; detection; computer-readable storage medium; polymorphic site; signal carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8299 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTTCTCCTGCCTTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8359 CICITCICCIGCCIGCCITTITGCTTTITCCICAIGACTCTTTTCTGCTCTTAAGAICAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 150; DB 12;
Local Similarity 100.0%; Pred. No. 8.8e-34;
tes 150; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rienhoff HY, Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8419 ATAATCCAGTTCATCCTAAAATGCTTTTTC 8448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MCP1 nucleotide sequence >MCP1_02.
                                                  Disclosure; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 74-75; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2002; 2002WO-US025268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACF64399 standard; DNA; 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2003 (first entry)
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  accumulation in eye.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DNAS-) DNA SCI INC
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WPI; 2002-130909/17
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                     The invention relates to single nucleotide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polypeptide. A method encoding human small inducible cytokine A2 (SCYA2) polypeptide. A method confront at the SCYA2 gene in a individual comprises identifying the for haplotyping at the copies of the gene is defined by one of the SCYA2 haplotypes given of the copies of the gene is defined by one of the SCYA2 haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotypes. An association between a pairs can be assigned to specific genotypes. An association between a crait and a haplotype or haplotype pair of the SCYA2 gene can be trait and a haplotype pair in a reference population, where a higher haplotype or haplotype or haplotype or papilotype or papilotype or papilotype or papilotype or papilotype pair in a reference population, where a higher haplotype or haplotype or haplotype or papilotype pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2 activity, such as
                                                                                                                                                                                                                                                                                                                                                                  1304 CAAAGAICACAITCIAGGCICIGAGGIAIAGGCAGAAGCACIGGGAITTAAIGAGGCICIII 1363
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiansemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisporiatic; antiantlammatoxy; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                CICTICICCIGCCIGCCITITICCICATGACTCTITICIGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                               CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                     Sequence 2775 BP; 699 A; 723 C; 565 G; 778 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                              Length 2775;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                     Score 146; DB 6; Le
Pred. No. 9.1e-33;
                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1424 ATAATCCAGTTCATCCTAAAATGCTTTT 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAATCCAGTTCATCCTAAAATGCTTTT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826
        Claim 1; Fig 1; 58pp; English.
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                                                                                                                                                                                                                                                                                                  97.3%;
98.6%;
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                                                                                                                                                                                                                                                                                                                             146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                    human SCYA2 polypeptide
                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CICITCICCIGCCIGCTITIGCTITITCCICALGACICITITICIGCICTIAAGAICAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 caaaaatcacatrctaactctaaaatataaacaaaaacacataaaatttaaaaactcttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAAGAICACAIICIAGCICIGAGGIAIAAGGCAGAAGCACIGGGAIIIAAAIGAGCICIII
fragment of chemically modified gene, useful for diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antiposriatic; antiantilleumatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disease; cytosine methylation; antiasthmatic; eriosclerotic; antianaemic; cytostatic; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5926 BP; 1554 A; 55 C; 1492 G; 2825 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                          Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune system associated gene SEQ ID NO: 1625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111.6; DB (
Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAATCCAGTTCATCCTAAAATGCTTTTC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL33652 standard; DNA; 5926
                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 84.0
Matches 126, Conservative
                   Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                          methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL33652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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5817
                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psociasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                       genetic variants having polymorphisms in the small inducible cytokine (SCYA2) gene, useful for studying the function of SCYA2, and for ating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                     61
 fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                 2 AAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                    TCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGAA
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, small inducible cytokine A2, SCYA2; gene, ds, haplotype pair, haplotyping, atherosclerosis, antiarteriosclerotic, gene therapy, single nucleotide polymorphism; genotyping, drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to single nucleotide polymorphisms in the gene
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                                                                                                                                                                                                                                      Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                German.
                                                                                                                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human small inducible cytokine A2 (SCYA2) modified DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee HH;
                                                               Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                      Score 92; DB 6; I
Pred. No. 7.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar AM,
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAATTTAGTTTATTTTAAATGTTTTTT 5905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 58; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koshy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK47980 standard; DNA; 840 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2000; 2000US-0228496P
                                                                                                                                                                                                                                                                    61.3%;
ilarity 76.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WO-US026899
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Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 17q11.2-q21.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-339655/37
                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002.
                                 methylation
                                                                                                                                                                                                                                                                                                      Matches 113;
                                                                                                                                                                                                                                                                                                                                                                   5758
                                                                                                                                                                                                                                                                                                                                                                                                                                  5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
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concoding human small inducible cytokine A2 (SCYA2) polypeptide. A method for haplotyping the SCYA2 gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the SCYA2 haplotypes given the copies of the gene is defined by one of the SCYA2 haplotypes given in the specification or whether both copies are defined by a haplotype capair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the SCYA2 gene can be can a population exhibiting the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype pair in a reference population, where a higher haplotype cor haplotype pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for sandidate drugs to treat diseases related to SCYA2, and in screening for sandidate drugs to treat diseases related to SCYA2 and in screening to shows the polymorphic sites in a uniform format to facilitate electronic searching of the SCYA2 haplotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining whether an individual is predisposed to susceptibility to low
bone mineral density (BMD) and/or bone damage, involves identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  low bone mineral density; BMD; bone damage; polymorphism; osteoporosis; single nucleotide polymorphism; SNP; gene; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method of determining whether an individual is predisposed to susceptibility to low bone mineral density (BMD) and/or bone damage comprising identifying whether the individual has at least one polymorphism in a polymoclectide encoding a protein, where the polymuclectide is one of 81 200-500 nuclectide sequences (S1, see ADC98215 to ADC98315). An agent identified in an method from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CAGAAGCACTGGGATTTAATGAGCTCTTTSTCTTCTCCTGCCTTTTGTTTTTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.7%; Score 58; DB 6; Length 840; 96.7%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 840 BP; 88 A; 115 C; 72 G; 138 T; 0 U; 427 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mangion J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townley DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphisms in associated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 225; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2002; 2002WO-US040948.
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ID ADC98306 standard; DNA; 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valdes A,
Schafer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-559156/52.
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Best Local Similarity
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Mckay I, 8
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by (GCA), by detecting the level of expression of comparing the DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are differential expression of Gs is indicative of GCA. Also included are modulating (MX) GA by contacting GC with an agent that alters the modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of a subject to a tissue, an allergic response in a subject, exposure of subject to a tissue, an allergic response in a subject, exposure of subject to a captones or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
present invention which can be used for the prevention or treatment of a disease resulting in susceptibility to low BMD and/or bone damage is useful in the manufacture of a medicament for use in modulating the susceptibility to low BMD and/or bone damage. The disease associated with low BMD and/or bone damage is osteoporosis. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 88; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; gearlie inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; acthms; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                               TCTTTTCTGCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA differentially expressed in granulocytic cells #68
                                                                                                                                                                                                            Length 201;
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                Sequence 201 BP; 59 A; 39 C; 46 G; 56 T; 0 U; 1 Other;
                                                                                                                                                                                                              DB 10; L
9.1e-06;
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                                                                                                                                                                                                       35.3%; Scott 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 68; 114pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                          35.3%
Query Match
Best Local Similarity 100.0
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                   98
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or expression or the gene is indicative or intrammation; (w) treating cresponse in a subject, exposure of a subject to a pathogen or sterile ciresponse in a subject, exposure of a subject to a pathogen or sterile ciresponse in a subject, exposure of a subject to a pathogen or sterile ciresponse in a subject, exposure of a subject to a sterile inflammatory disease, by contacting a tissue having inflammation with an odetecting GGA, M2 is useful for modulating GA, M3 is useful for detecting an agent capable of modulating GCA preferably in a confinemation in a tissue; M4 is useful for detecting an inflammation in a tissue; M4 is useful for detecting an inflammation of inflammation in a tissue, an allergic response in a subject of exposure of a subject to a pathogen or sterile inflammatory disease (e.g. corditally chronic) in a tissue, an allergic response in a subject of septimation in a tissue, and allergic response in a subject of cardiac reperfusion injury, renal reperfusion injury, ARDS, adult of cardiac reperfusion injury, renal reperfusion injury, periodontal disease, alcerative collitis, periodontal disease; also bacterial of disease, ulcerative collitis, periodontal disease; also bacterial of unfection, that infection, parasitic infection, protozzal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially not may art of the printed specification, but was obtained in clearnoic format directly from WHPO at this patent did electronic format directly from WHPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GATITAAIGAGCICTITICICTICCTGCCTGTTTTGCTTTTTCCTCATGACTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 227968 BP; 53185 A; 60440 C; 61985 G; 52358 T; 0 U; 0 Other;
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gene is indicative of inflammation; (4)
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Pred. No. 10;
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57.9%;
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The invention relates to polypeptides, comprising at least an optionally untated amino acid sequence AAG78184-AAG78187 and having c-kit gene promoter controlling activity, especially in mast cells. The polypeptides are useful in diagnosing disease associated with mast cells and controlling MITF (microphtsalmia-associated transcription factor) and the MITF gene, especially in mast cells. The present sequence is that of a MITF protein isoform encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides that control MITF and MITF gene in mast cells for use in
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              Mouse MITF-origin protein isoform encoding cDNA SEQ ID NO
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                                                     Mouse; MITF; origin; c-kit; mast cell; microphtalmia-associated transcription factor; ss
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122. .1534
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Best Local Similarity 54.99
Watches 67; Conservative
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated but he invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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fragments
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The invention relates to polypeptides, comprising at least an optionally mutated amino acid sequence AAG78184-AAG78187 and having c-kit gene promoter controlling activity, especially in mast cells. The polypeptides are useful in diagnoshing disease associated with mast cells and controlling MITF (microphtalmia-associated vith mast cells and HTF gene, especially in mast cells. The present sequence is that of a MITF protein isoform encoding cDNA
                                                                                                                                                               Polypeptides that control MITF and MITF gene in mast cells for use in a related medical area.
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08-MAR-2000; 2000JP-00063959
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Job time: 104.413 secs
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P-PSDB; AAG78184.
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59. .1663
/*tag= a
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                                                                                                            07-MAR-2001; 2001WO-JP001752
                                                                                                                                                   08-MAR-2000; 2000JP-00063959
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146

98

Gaps .; 0

Length 2196; 55; Indels

DB 4;

Score 34; DB 4 Pred. No. 6.3; 0; Mismatches

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Homo sapiens (human)
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nRNA sequence.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                               BG109427/c
                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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 ORIGIN
  BU358171 60358157
BH355897 CH230-199
AZ117778 RPCI-23-4
AZ094475 RPCI-23-4
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CC474603 tigr-G88-
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BU276566 603866116
CC141545 EST836216
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8064.741 Million cell updates/sec
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      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                    34239544 seqs, 19032134700 residues
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Listing first 45 summaries
                               - nucleic search, using sw model
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BG109427 150 bp mRNA linear BST 30-JAN-2001
602280491F1 NIH_MGC_86 Homo sapiens CDNA clone IMAGE:4367999 5',
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLMM10021 row: e column: 24
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Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BU368195
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24.7%; Score 37; DB 4; Length 750;
Best Local Similarity 67.5%; Pred. No. 15;
Matches 52; Conservative 0; Mismatches 25; Indels
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Location/Qualifiers
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BG109427.1 GI:12602933
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1 (Geer, K., D., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., D., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Rigges, F., de Jong, P. and Fraser, C.M. CHORI-230 EcoRI segment Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)

Ochtace: Shaying Zhao
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
1712 Medical Center Dr., Rockville, MD 20850, USA
1721 Medical Center Dr., Rockville, MD 20850, USA
1731 Medical Center Dr., Rockville, MD 20850, USA
1731 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                    660 bp DNA linear GSS 03-DEC-2001
CH230-199118,TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-199118, genomic survey sequence.
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91 TCATGACTCTTTTCTGCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTTC 150
                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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RPCI-23-478J14.TJ RPCI-23 Mus musculus genomic clone
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/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
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/clone="CH230-199118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
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/clone_11b="CSECRCRN73"
/clone_11b="CSECRCRN73"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: million independent clones. cDNA
constructed from 1 million independent clones. cDNA
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
Following this first strand caction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
was blunted, ligated to NotI adapters of the compartible sites of a custom modified MCS of the
compartible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
pBluescript (KS+) vector adapted from Soares et al., PNAS
(1994) 91: 928-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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Gallus gallus
Gallus gallus
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

1 (basea 1 to 750)
Boardman, P.E., Sanra-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Gurr. Biol. 12 (22), 1965-1969 (2002)
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603568157F1 CSEQCHN73 Gallus gallus CDNA clone ChEST524a16 5', mRNA
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                                            CIGGGATITAATGAGCICTITCTCTTCTGCCTGCCTTTTTGCTTTTTCCTCATGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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/dev_stage="adult"
/lab_nost="DH10B"
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larity 56.7%; Pred. No. 17;
Conservative 0; Mismatches
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/organism="Gallus gallus"
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/strain="Compton Line 15!"
/db_xref="teaxon:9031"
/clone="ChEST524a16"
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PO Box 88, Manchester, M60 10D, UK
PO Box 88, Manchester, M60 10D, UK
Par: 01612260409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. 1 (bases 1 to 522)
E. 1 (bases 1 to 522)
Akinret, B., Levins, M., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-478J14.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
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Seq primer: SP6
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RPCI-23-478J14, genomic survey sequence.
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iive 0; Mismatches
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AQ994475

564 bp DNA linear GSS 24-FEB-2000
RPCI-23-270M5.TJ RPCI-23 Mus musculus genomic clone RPCI-23-270M5, genomic survey sequence.

AQ994475/c LOCUS

RESULT

DEFINITION

ACCESSION

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tigr-gss-dog-17000335613614 Dog Library Canis familiaris genomic, genomic survey sequence. CR406656.1 GI:36659452 GSS.
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Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 564)
Zhao,S., Nieman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Opubblished (1999)
Other_GSSS: RPCI-23-270M5.TV
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/clone_lib="RPCI-23"
/note="Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: 9210-020.

Email: 9210-020.

Clones are derived from the mouse BAC library RPCI-23. For BAC clones are derived from the mouse Clones may be purchased from (pieteredejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 270 row: M column: 5

Seg primer: 8P6

Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .564
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-270M5"
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CE406656
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547

SOURCE

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Populus balsamifera subsp. trichocarpa x Populus nigra Populus balsamifera subsp. trichocarpa x Populus nigra Populus balsamifera subsp. trichocarpa x Populus nigra Bukaryota; Viridiplantae; Streptophyta; Envrophyta; Tracheophyta; Sprematophyta; Greendicot; Sarematophyta; Manoliophyta; endicotyledons; core endicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus. 1 (bases 1 to 643)
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Unpublished (2004)
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Genome BC forest genomics program
University of British Columbia
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-6097
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/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone_lib="Dog_Library"
/note="Site_1: Bstx1; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                              v Match 24.0%; Score 36; DB 9; Length 706; Local Similarity 54.5%; Pred: No. 27; Conservative 0; Mismatches 60; Indels
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plate: WS02018 row: K column: 16
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|mol type="mRNA"
|cultivar="NxM6"
|db_xref="taxon:293756"
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
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CV262112.1 GI:52515087
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Lontact: Kirkness EF
Lontactitute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 bp DNA linear GSS 30-SEP-2003 tigr-gss-dog-17000330621810 Dog Library Canis familiaris genomic, CR774601
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(Dases 1 to 706)

Kirkness; E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Riskness; E.F., Bafna, V., Halpern, A.B., Veraser, C.M. and Messer, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                             Canis familiaris herbrata; Craniata; Vertebrata; Euteleostomi; Bukraryota; Merazoa; Chordata; Crania; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 706)

Rixheness E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AGATCACATTCTAGGTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AAAİGGTALCATAĞÇAÇATATĞIRĞTATAÇAACÇİTĞCTİÇTİTTĞTİÇİTİĞİT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                       The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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24.0%; Score 36; DB 9; Length 706;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 69; Conservative 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: shotgun.
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14512627
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DEFINITION
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VERSION
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SOURCE
ORGANISM
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AUTHORS
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JOURNAL
MEDLINE
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COMMENT
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CE774603
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JOURNAL
MEDLINE
PUBMED
COMMENT
                                                                            ORGANISM
                                                                                                                                                          REFERENCE
                                                                                                                                                                                  AUTHORS
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/cell_type="Blood"
/clone_lib="TAMBT"
/note="Vector: pBeloBACI1; Site_1: HindIII; Site_2:
HindIII; TAMBT Bovine BAC library (Male) produced by Texas
A&M University, Department of Animal Science."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.7%;
Best Local Similarity 53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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BU854111
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/clone_lib="PTXN-IB-N-A-11"
/clone_lib="PTXN-IB-N-A-11"
/clone_lib="PTXN-IB-N-A-11"
/clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC927097 740 bp DNA linear GSS 08-AUG-2003
t093j2lba.fl TAMBT Bos taurus genomic clone t093j2lba, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 FCATGACTCTTTTCTGCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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/strain="Angus bull T A M U Shoshone Y6 11519666"
/db_xref="taxon:9913"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.9%; Score 35.8; DB 7; Length 643; Best Local Similarity 56.3%; Pred. No. 31; . . . Matches 67; Conservative 0; Mismatches 52; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 530.
Location/Qualifiers
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clone="WS02018 K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gurvey sequence.
CC927097
CC927097.1 GI:33562436
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ORGANISM
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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749 bp mRNA linear EST 16-OCT-2002
AGENCOURT_10402929 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6621266
5', mRNA sequence.
BU854111
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                                                                                  50 ATGAGCTCTTTCTCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTC 109
                                                                                                                          258 AIGGTCAGTTTCCCTTCTCAIGCCTGCACTTCGTTCTTTCCTAAAGCTTCTGGAGGAGTG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 749)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2872 row: 1 column: 02
High quality sequence stop: 585.
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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  Length 740;
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Score 35.6; DB 9; Length 7. Pred. No. 35; 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64; Indels
                                                                                                                                                                   110 TTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTT 147
                                                                                                                                                                                         198 TTTGCATCAGGAAATCCAGAGGAGCAGAGGCTGCTAT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.6; DB 5;
Pred. No. 36;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    BU854111.1 GI:24039077
ch 23.7%;
1 Similarity 60.2%;
59; Conservative
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1. .491

/organism="Gallus gallus"

/mol type="mkNa"

/mol type="mkNa"

/strāin="Leghorn and broiler"

/db xref="taxon:9031"

/clone="agaL 27P09"

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/lab host="agAL 57P09"

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/clone lib="BARC 3GAL chicken mixed tissue"

/clone="agaL 2P08"

/clone lib="BARC 3GAL chicken mixed tissue"

/clone lib="BARC 3GAL chicken mixed tissue"

/clone lib="bara" ultimobranchial gland, parathyroid

from whole brain, ultimobranchial gland, parathyroid

gland, cecal tonsil and primordial germ cells Multiple"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 bp mRNA linear EST 26-JUN-2003 4039997 1GAL - Chicken Intestinal Lymphocyte Gallus gallus CDNA clone iGAL 7D16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Calliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 546)
Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van
Tassel, C. and Han, J.Y.
Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function
Unpublished (2003)
                                                                                                                                                                                                                                                                                  Party 2016/86224

Fax: 3015048623

Fax: 3015048623

Bmaail: chriscGemiri.barc.usda.gov

Bmaail: chriscGemiri.barc.usda.gov

Bases called and trimmed with phred

Bingle pass sequencing. Bases called and trimmed vith phred

0.00025 using options -trim_alt ', -trim_fastaVector identified by

0.00025 using options -minmatch 12 -minscore 12

Plate: 77 row: P column: 09

Seq primer: CCCAGTACGACGTTGTAAAACG

High quality sequence stop: 491.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinee; Gallus.

1 (bases 1 to 491)

Evock-Clover, C.M., Ashwell, C.M., McMurtry, J.P., Lillehoj, H.S., Matukumalli, L.K. and Van Tassell, C.P.
Characterization of expressed sequence tags generated from multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 †GATCAGTCCGTTCAACTCCTTGAAAAAAAAAGGCCATTCCTTCTTAAAGGCCAATTCCTTAAAAGTTTTTTT
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                                                                                                                                                                           Unpublished (2004)
Contact: Christina M. Clover
Contact: Christina M. Clover
Growth Biology Laboratory
Animal and Natural Resources Institute
Animal and Natural Resources
Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
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Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Animal and Natural Resources Institute, TSDA
Animal and SARC-East, Beltsville, MD 20705, UT 201: 3015048771
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1 Similarity 56.4%; Pred. No. 38;
66; Conservative 0; Mismatches
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                                                                                                                                                               chicken tissues
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                                                                      REFERENCE
AUTHORS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sterky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P., Sterky, F., Bhalerao, R.R., Jonsson-Lindvall, J., Tandre, K., Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P., Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, J. and Jansson, S. A Populus EST resource for functional genomics Unpublished (2003)
Other ESTS: 1014P80P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK094148 Linear EST 01-DEC-2003 1014P80.3pR Populus senescing leaves cDNA library Populus tremula CDNA clone 1014P80 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embryophyta; Tracheophyta;
                                                                                  70 IGCCIGCCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGAATAATCCAG 129
                                                                                                         328 CICAGITCITITAGITICCICICITITIGACATAAICIGGGITITIAGIA 387
                                     268 CATIGAAGAIGGGAGAGAGTAGCCTGAGAACTGACCTTTTCTGITCTGAGTCTGAGCTTC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus tremula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 434)
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/db_xref="taxon:113636"
/dl_one="104808"
/tiseue type="Senescing leaves"
/clone_lib="Populus senescing leaves cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Umea Plant Science Center, Department of Plant Physiology
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Pred. No. 38;
0; Mismatches 36;
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/organism="Populus tremula"
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Tel: +46 90 786 5279
Fax: +46 90 786 6576
Email: bo.segerman@plantphys.umu.se.
Location/Qualifiers
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                                                                                                                                                                                                              CK094148.1 GI:38578473
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23.6%;
Best Local Similarity 61.3%;
Matches 57; Conservative (
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CK094148/c
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus

1 (bases 1 to 638)
El (bases 1 to 638)
Stranglus, Metallus, Metazinger, V., Desert, C., Retout, E., Piumi, F., Klopp, C. and Douaire, M.
Construction and primary characterization of chicken normalized
uniti-issue cDNA libraries
Unpublished (2003)
On Feb 27, 2003 this sequence version replaced gi:28592193.
On Feb 27, 2003 this sequence version replaced gi:28592193.
On Feb 27, 2003 this sequence version replaced gi:28592193.
Feb 27, 2003 this sequence version replaced gi:28592193.
Feb 27, 2003 this sequence version replaced gi:28592193.
On Feb 27, 2003 this sequence version replaced gi:28592193.
Feb 27, 2003 this sequence version replaced gi:28592193.
Feb 27, 2003 this sequence version replaced gi:28592193.
Feb 23, 408 54 54 70
Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX269592 AGENAE Gallus gallus multi-tissues normalized library (gcag) Gallus gallus clone gcag0019c.1.12 3prim, mRNA
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/tissue_type="multi-tissues"
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/mol_type="mRNA"
/db_xref="taxon:9031"
                   /sex="Male and female"
/dev stage="adult"
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clone="ChEST959£18"
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Matches 66; Conserv
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BX269592/c
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (baes 1 to 626)
Boardann, P.E., Sanz-Erquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
         Email: hilleho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options trim_alt ' '-trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 7 row: D column: 16
Seq primer: ATTAGGTGACAATAAG
High quality sequence stop: 546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="1GAL - Chicken Intestinal Lymphocyte" /note="0rgan: Intestine; Vector: pGWY-SPORT6; Site 1: Sall; Site 2: Not1; Normalized library from chicken gut infected wIth coccidia duodenum and middle gut."
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University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.6%; Score 35.4; DB 6; Length 546; Best Local Similarity 56.4%; Pred. No. 39; Matches 66; Conservative 0; Mismatches 51; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/mol type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                           /mol_type="mRNA"
/mol_type="white leghorn SC"
/db_xref="taxon:9031"
/clone="1GAL_7D16"
/sex="mixed"
                                                                                                                                                                                                                     organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Gut"
/cell_type="Lymphocyte"
/dev_ftage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BU492000
BU492000.1 GI:25985577
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Fax: 01612360409
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August 4, 2005, 07:01:49; Search time 30.9109 Seconds (without alignments) 7940.282 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES	ΙD	US-08-916-421B-1	US-09-692-570-1	US-09-949-016-15630	US-09-949-016-152710	US-09-949-016-16029	US-09-949-016-12511	US-09-949-016-13725	US-08-232-463-14	US-09-949-016-16423	US-09-949-016-16994	US-09-328-925-4	US-09-949-016-16308	US-09-949-016-12928	US-09-949-016-12740	US-09-949-016-4716	US-09-949-016-191	US-09-949-016-16458	US-09-949-016-11933	US-09-949-016-13614	US-09-949-016-15358	US-09-949-016-11750	US-09-949-016-16934	US-08-181-629A-3	US-08-181-629A-2	US-09-949-016-16105	US-09-949-016-70039	US-09-949-016-16845
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## ALIGNMENTS

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Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocorpation of 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-09-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
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ORGANISM: Methanococcus jannaschii
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
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LOCATION: (98120)..(98120)
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OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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LOCATION: (84773)... (84773)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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LENGTH: 1664976
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NAME/KEY: misc\_feature

ö 46 TITAATGAGCTCTTTCTCTTCTCCTGCCTTTTTGCTTTTTTCCTCATGACTCTTTTCT 105 Gaps Query Match 23.1%; Score 34.6; DB 4; Length 1664976; Best Local Similarity 58.1%; Pred. No. 4.4; Matches 61; Conservative 0; Mismatches 44; Indels 0; 397084 ATCATCATRATCATCATCATCATAATCATAATCCTCTTC 397040 106 GCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTTC 150 NAME/KEY: misc feature LOCATION: (1664854)..(1664855) OTHER INFORMATION: n equals a, t, c, or g US-08-916-421B-1 ຫ מ ρ മ þ б b ρ δ b ρ p Ø b or or or or c, or or or ör or or ŏ or or ö or ö ö ů ΰ ů ΰ ΰ ΰ ບັ ϋ ΰ ບັ ပဲ ú ΰ RESULT 2 US-09-622-570-1/c 'Sequence 1, Application US/09692570 ; Patent No. 6797466 NAME/KEY: misc\_feature LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, t, ú INFORMATION: n equals a, t, ú ن ú NAME/KEY: misc feature
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NAME/KEY: misc\_feature
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OTHER INFORMATION: n equals a, t, NAME/ACIT INTELLIGENCE OF THE NAME/ACIT ON COTHER INFORMATION: n equals a, t, NAME/ACIT ON COTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, NAME/ACIT (1119881) CHER INFORMATION: n equals a, t, NAME/ACIT (1130881). (1130881) COTHER INFORMATION: n equals a, t, NAME/ACIT (1130881). (1130881) COTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (855539)..(855539) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (871519)..(871619) OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (1470091,...OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (779676)...(779676)
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LOCATION: (682442)..(682442)
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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234220)..(234220)
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992) ..(600992)
OTHER INFORMATION: n equals a, t,
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LOCATION: (309418)..(309418)
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LOCATION: (559241). (559241)
OTHER INFORMATION: n equals a,
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FEATURE:
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OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
OTHER INFORMATION: n equals
                                      NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals
              APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
TITLE OF INVENTION: Jannaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR PILING DATE: 1996-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTING DATE: 1997-08-32
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTING DATE: 1997-08-32
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTING DATE: 1997-08-32
NUMBER OF SEQ ID NOS: 20
LENGTH: 1664976
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a,
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LOCATION: (28222)
OTHER INFORMATION: n equals a,
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
GENERAL INFORMATION:
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RESULT 4

US-09-949-016-152710

J Sequence 152710, Application US/09949016

Sequence 152710, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINHER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 601
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 rrcakcrakrrrrgrrrccrcrcrccrccrrccacrcccrrrcrgrccrcrrcrrcrrr 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%; Score 33.8; DB 4; Length 1 60.2%; Pred. No. 2.7; tive 0; Mismatches 37; Indele
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                              PILE BEFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREEEEG for Windows Version 4.0
SEQ ID NO 15630
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(112705)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-15630
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Query Match
Best Local Similarity 58.6
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.2
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
; ORGANISM: Human
US-09-949-016-152710
                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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LOCATION: (1349473)...(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, C,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, FRATURE:
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t,
FEATURE:
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
                                                                    NAME/KRY: misc feature
LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a.
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NAME/KEY: misc feature
LOCATION: (871619)
OTHER INFORMATION: n equals a,
FEATURE:
                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (779455)
OTHER INFORMATION: n equals a,
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US-09-99-016-15630
US-09-99-016-15630, Application US/09949016
Sequence 15630, Application US/09949016
Patent No. 6812339
Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

RESULT 3

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US-09-949-016-13725/c
; Sequence 13725, Application US/09949016
; Baten No. 681239
; GENERAL INFORMATION:
; PAPLICANT: VERYER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CL001307
; CURRENT APPLICATION NUMBER: 05/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR REPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NO 13-25
                                                                                                      98488 TGGGTTTTTATTTCTTCTTCTTCTTCTTCTGCCTTTGTTTTTTCTTTTCCTCTGAGTGT 98429
                                                 41 TGGGATTTAATGAGCTCTTTCTCTTCTGCCTGCCTTTTTGCTTTTTCCTCATGACTCT 100
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  Gaps
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23; Indels
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
APPLICANT: DORNER, F.; APPLICANT: SCHEIFLINGER, F.; APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 5.2
; CORRESPONDENCE ADDRESS:
ADDRESSEBE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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  Mismatches
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Pred. No. 4;
0; Mismatches
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(100468)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13725
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22.1%;
Best Local Similarity 67.1%;
Matches 47; Conservative
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47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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  Matches
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                                                                                                                    APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR APPLICATION NUMBER: 60/231,498

FRIOR APPLICATION NUMBER: 60/231,498

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WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

FRIOR FILING DATE: 2000-09-08

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREEKSEQ for Windows Version 4.0
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98206 TTCAACTAGTFTGTTTCCTCTCTCCTTTCCACTCCCTTTCCCTTCTGCTCTTTTT 98265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.4; DB 4; Length 155019; Pred. No. 4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
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Pred. No. 4;
                                               Sequence 16029, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12511, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                b LOCATION: (1)._.(155019)
c OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%;
58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.3
Best Local Similarity 58.6
Matches 58; Conservative
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LOCATION: (1)...(10046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 16029
LENGTH: 155019
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LENGTH: 100463
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   Indels
      63;
      0; Mismatches
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Best Local Similarity 58.3%
The Tile Conservative
Tile Conservative
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             Conservative
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US-09-949-016-16994
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                10;
                Matches
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| Sequence 16423, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER
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                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 39,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 39,768
TELEPROMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPRAK: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.5%; Score 32.2; DE Best Local Similarity 13.1%; Pred. No. 2.9; Matches 19; Conservative 74; Mismatches
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Pred. No. 10;
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52.6%;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: 81ngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , CLONE: PTZGPt-F1s
US-08-232-463-14
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-16423
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Sequence 16094, Application US/09949016
; Sequence 16094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANTY VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
    TORRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR PLING DATE: 2000-10-20
    PRIOR PLING DATE: 2000-10-03
    PRIOR PLING DATE: 2000-10-03
    PRIOR PLING DATE: 2000-10-03
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Sequence 4, Application US/09328925

Sequence 4, Application US/09328925

Sequence 7, Application Sequences

APPLICANT: Kurachi, Kotoku
APPLICANT: Kurachi, Sumiko
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
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                                                                                                                         68846 CTATGATTTTTTCCAGTTTTTAGGAGTACGTAGAGTTTTTCCATGTAACTGGGCTCATT 68905
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                                                                                                                                                                                                                                                          61 CTCTTCTCCTGCCTGTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
1 CAAAGAICACATITCIAGCICTGAGGIATAGGCAGAAGCACTGGGATITAAIGAGCICTII
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: (10/19/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: (60/241,755
PRIOR PELICATION NUMBER: (60/241,756
PRIOR PELICATION NUMBER: (60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2010-12
SOSTWARER FREESEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12740, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
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    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. CRAIG et al.
    APPLICANT: VENTER, J. CRAIG et al.
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    APPLICANT: VENTER, J. CRAIG et al.
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0; Mismatches
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PRIOR APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.2%; Score 31.8; Best Local Similarity 64.0%; Pred. No. 15 Matches 48; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31.8;
Pred. No. 15
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OTHER INFORMATION: n = A,T,C or G
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THER INFORMATION: n = A,T,C or G
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64.0%;
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Best Local Similarity
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US-09-949-016-12740
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ORGANISM: Human
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LENGTH: 194537
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Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-0-08

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESOF for Windows Version 4.0
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                                                                                                                                                                 DB 4; Length 38059;
                                                                                                                                                                                                                                          50; Indels
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                                                                                                                                                         Query Match 21.3%; Score 32; DB 4
Best Local Similarity 58.9%; Pred. No. 6.6;
Matches 73; Conservative 0; Mismatches
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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OTHER INFORMATION: n = A,T,C or G
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Matches 75; Conservative
    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-4
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LENGTH: 48691
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Qy 1123 AATCCACTTCAGCTT 117210

Bb 117196 GAGCAACTTCAGCTT 117210

Bb 117196 GAGCAACTTCAGCTT 117210

Bb 117196 GAGCAACTTCAGCTT 117210

RESULT 15

US-09-949-016-4716

SQUERCA 4716

STILE REPERENCE: CLO01307

CURRENT APPLICANT: WITH HUMAN DIBEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DIBEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF THE PELLOS DATE: 2000-04-14

STILE REPERENCE: CLO01307

CURRENT APPLICANTION NUMBER: US/09/949,016

STILE REPERENCE: CLO01307

CURRENT APPLICANTION NUMBER: US/00/949,016

STILE REPERENCE: CLO01307

CURRENT APPLICANTION NUMBER: US/00/949,016

SPICE RELIAGO DATE: 2000-06-04

SPICE RELIAGO DATE: 2000-06-05

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                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

US-09-899-276-3	US-10-044-090-839	US-10-685-705-4	US-10-833-656-2	US-10-311-455-1626	US-10-311-455-1625	US-10-723-860-1357
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33.6 22.4 81684 19 US-10-122-281-67 33.4 22.3 603 13 US-10-027-632-10 33.4 22.3 603 13 US-10-027-632-10 33.4 22.3 603 17 US-10-027-632-10 33.4 22.3 603 17 US-10-027-632-10 33.4 22.3 603 17 US-10-027-632-10 33.4 22.3 603 17 US-10-027-632-10 33.4 22.3 603 17 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 33.4 22.3 754 13 US-10-027-632-10 32.8 22.3 754 17 US-10-027-632-10 32.4 21.6 637 11 US-10-027-632-10 32.4 21.6 637 13 US-10-027-632-10 32.4 21.6 637 13 US-10-027-632-10 32.4 21.6 637 13 US-10-027-632-10 32.4 21.6 637 13 US-10-027-632-10 32.4 21.6 637 13 US-10-027-632-10 32.4 21.6 637 17 US-10-027-632-10 32.4 21.6 637 17 US-10-027-632-10 32.2 21.3 736 11 US-10-027-632-10 32.2 21.3 736 11 US-10-027-632-10 32.2 21.3 736 11 US-10-027-632-10 32.2 21.3 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	33 6 22 4 81	10 33.4 6 222.3 11 12 33.4 6 222.3 11 12 33.4 6 222.3 11 12 33.4 6 222.3 12 12 12 12 12 12 12 12 12 12 12 12 12	14 33.4 22.3 16 33.4 22.3 18 33.4 22.3 19 33.4 22.3 10 10 10 10 10 10 10 10 10 10 10 10 10	22 33.2 22.3 33.2 22.3 22.3 22.3 22.3 2	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1  'Sequence 3, Application US/0  'Batent No. US20020106355A1  'GENERAL INFORMATION:  'APPLICANT: Ros1, Frank  'APPLICANT: COY, Johando  'APPLICANT: COY, Johannek  'APPLICANT: Pinzer, Patrick  'APPLICANT: Poustex, Annema  'APPLICANT: Pinzer, Patrick  'APPLICANT: Poustex, Annema  'APPLICANT: Poustex, Annema  'APPLICANT: Poustex, Hancen, Har  'APPLICANT: Patzelt, Andrea  'TITLE OF INVENITON: No. US2  'TITLE OF INVENITON: No. US2  'CURRENT APPLICATION NUMBER:  CURRENT TILING DATE: 2001-  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF SEQ ID NOS: 12  'NUMBER OF	al Simi 150;

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Query Match
Best Local Similarity 100.0%;
Matches 150; Conservative 0;
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NAME/KEY: misc feature
LOCATION: (2583) .. (2583)
OTHER INFORMATION: n = c, a
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LOCATION: (2582)..(2582)
OTHER INFORMATION: n = C,
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; ORGANISM: Homo sapiens
US-10-685-705-4
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US-10-833-656-2
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; Sequence 4, Application US/10685705
; Publication No. US20040177387A1
; GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Ambati
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR PLILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 11793
                                                                                                                                                                                                                                                              | Sequence 839, Application US/10044090 |
| Sequence 839, Application No. US20020137081A1 |
| CENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL US/10/044,090 |
| TITLE OF INVENTION: GENERAL US/10/044,090 |
| CURRENT PELING DATE: 2002-01-09 |
| NUMBER OF SEQ ID NOS: 850 |
| SEQ ID NO 839 |
| SEQ ID NO 839 |
| LENGTH: 724
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                                                                        CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
     CAAAGATCACATTCTAAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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Best Local Similarity 100.0%; Pred. No. 6.1e-37;
Matches 150; Conservative 0; Mismatches 0; Indels 0
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OTHER INFORMATION: Incyte ID No. US20020137081A1 1075405.1
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                                                                                                                                                  121 ATAATCCAGTTCATCCTAAAATGCTTTTTC 150
                                                                                                                                                                          NAME/KEY: unsure
LOCATION: 677, 710
CTHER INFORMATION: a, t, c, g, or other
US-10-044-090-839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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US-10-044-090-839
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APPLICANT: Wandl, Roman
APPLICANT: Doods, Henri
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Seidler, Randolph
TITLE OF INVENTION: Chemotactic factor
FILIE REPRENCE: Case 1/140/833,656
CURRENT APPLICATION NUMBER: US/10/833,656
CURRENT FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 2776
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                                      0; Gaps
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Length 11793;
    Score 150; DB 19;
Pred. No. 1.7e-36;
Mismatches 0;
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                                             0; Mismatches
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LOCATION: (2585)..(2585)
OTHER INFORMATION: n = c, a, t or 9
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Sequence 1357, Application US/10723860
; Publication No. US20040253606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Aliaburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions (TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators CURRENT APPLICATION WUMBER: US/10/723,860
CURRENT PILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5758 AAAGATTATATATTTTAGTTTTTGAGTATAGGTAGAAGTATTGGGATTTAATGAGTTTTTG 5817
                                                                                                                                                                                                                                                                               103
                                                                                                                                                                                                                              62 ICTTCTCCTGCCTGCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGAA 121
                                                                                                                   2 AAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTC
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                                                      Gaps
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DB 15; Length 5926;
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APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morel
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SEQ ID NO 673
LENGTH: 81684
Score 92; DB 15; Length 59
Pred. No. 2.5e-18;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        5878 raartragrirarrraaaargririr 5905
                                                                                                                                                                                                                                                                                                                                               122 TAATCCAGTTCATCCTAAAATGCTTTTT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
Query Match
Best Local Similarity 76.4%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (1)...(81684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens
US-10-723-860-1357
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US-10-723-860-1357/c
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LENGTH: 227968
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                              Sequence 1656, Application US/10311455

Sequence 1656, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: UNDER: US/10/311,455

CURRENT APPLICATION NUMBER: DI0/311,455

CURRENT FILING DATE: 2001-07-02

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1626

LENGTH: 5926
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Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: DIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by TILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by PILOR REPERBRICS: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
LENGTH: 5926
                           -10-311-455-1626/c
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US-10-311-455-1625
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58.6%;
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Best Local Similarity 58.6
Matches 58; Conservative
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US-10-027-632-105898
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Sequence 105897, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

Publication No. US20020198371A1

GENERAL INFORMATION:

Publication No. US20020198371A1

GENERAL INFORMATION:

Publication Interved General Carlow of General Carlow of TITLE OF INVENTION:

PITLE OF INVENTION:

POLYMERY APPLICATION UNMERS: US 60/218,006

PRIOR FILING DATE: 2002-04-30

CURRENT FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/189,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 1000-04-20

PRIOR PILING DATE: 1000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                               Length 81684;
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                                                                                                                                                                         Indels
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                                                                                                          DB 19;
                                                                                                          22.4%; Score 33.6; DB 19;
59.4%; Pred. No. 16;
tive 0; Mismatches 39;
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; Sequence 105898, Application US/10027632
; Publication No. US20020198371A1
, OTHER INFORMATION: n = A,T,C or G US-10-322-281-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.6
Matches 58; Conservative
                                                                                                                     Query Match
Best Local Similarity 59.4'
Matches 57; Conservative
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US-10-027-632-105897/c
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US-10-027-632-105897
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Pred. No. 3.1;
0; Mismatches 41;
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-09-09-09
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PRIOR FILING DATE: 199
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219 TICAACTAGTITIGITICCTCTCCTCCCTTCCACTCCCTTTTCCTTTTT 160
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                                                                                                                                                                                                                                                        Sequence 105897, Application US/10027632

Publication No. US2003020407539

Publication No. US2003020407539

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: PolyMorphisms in the Human Genome

FILE REPERENCE: 108027, 129

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/219,006

PRIOR PELING DATE: 2000-00-12

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PELING DATE: 1999-01-23

PRIOR PELING DATE: 1999-01-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PELING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR PELING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PELING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-08-08

SOFTWARE PERSENG FOR WINDOWS VERSION 4.0

SEQ ID NO 105897
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Publication No. US2030204075A9;
Fublication No. US2030204075A9;
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Polymorphisms in the Human Genome;
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
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Pred. No. 3.1;
0; Mismatches 41; Indels 0
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Best Local Similarity 58.6%;
Matches 58; Conservative
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US-10-027-632-105897/c
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US-10-027-632-105898/c
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US-10-027-632-105897
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Pred. No. 3.1;
0; Mismatches 41;
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Pred. No. 3.1;
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PLLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREUSE FOR WINDOWS VETSION 4.0
SEQ ID NO 105898
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58.6%;
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Best Local Similarity 58.6
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Conservative
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Best Local Similarity
Matches 58; Conserv
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US-10-027-632-105898
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US-10-027-632-105899
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US-10-027-632-19185/C

US-10-027-632-19185/C

Sequence 19185, Application US/10027632

Sequence 19185, Application US/2002033

Publication No. US20020199371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION: POLYMORPHISM in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/184,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1090-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 19185

LENGTH: 754

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Job time : 268.571 sec8
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CRGANISM: Human
US-10-027-632-19185
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AC118224 Mus muscu
AC13046 Mus muscu
AC094776 Rattus no
AC133423 Rattus no
BX897729 Zebrafish
CR589944 Danio rer
AC113063 Mus muscu
BX927324 Danio rer
AC113063 Mus muscu
BX927727 Rattus no
AC104727 Rattus no
AC10472 Homo sapi
AC05610 Homo sapi
AC150055 Gallus ga
AC150055 Gallus ga
AC150055 Gallus ga
AC132785 Rattus no
AC132785 Rattus no
BV051306 S212P6022
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         AC113256 Rattus no
AC111054 Mus muscu
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 8.4e-70;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 4 from Patent EP1170372.
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AC0467046

AC033423

BX897729

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AC133063

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Matches 250; Conservative
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D26687 Human gene
Y18933 Homo sapien
AC055549 Homo sapien
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L32659 Bovine mono
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(1) sites for [Unpublished (1989) Dana-Farber Cancer Inst., Boston, Ma., 02115]. Kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Coganism="Homo sapiens" ("Organism="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo sapiens" "Amol type="Homo 
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Human JE gene encoding a monocyte secretory protein, exon 1.

M28223 M26035

M28223.1 G1:338003

Secretory protein.

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Homo sapiens (human)

Homo sapiens
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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2 (Stier, P., Brnst, T. and Wong, G.G. The human homolog of the JE gene encodes a monocyte secretory protein
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Matches 250; Conservative 0; Mismatches 0;
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Original source text: Human WI-38 embryo lung fibroblast DNA, clone hJE-34, passage 14.
Location/Qualifiers
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cytokine; secretory protein.

cytokine; secretory protein.

Homo aspiens (human)

Homo sapiens

Evaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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Rollins,B.J., Stier,P., Ernst,T. and Wong,G.G.

The human homolog of the JE gene encodes a monocyte secretory
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Human monocyte secretory protein (JE) gene, exon 1.
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Methods for assessing and treating leukemia
Methods (MO 03038129-A 95 08-MAY-2003;
Patent: WO 03038129-A 95 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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Matches 250; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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Sequence 95 from Patent WO03038129.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Rollins,B.J., Stier,P., Ernst,T. and Wong,G.G.
The human homolog of the JE gene encodes a monocyte secretory
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MCP-1; monocyte chemoattractant protein-1.
Homo sapiens (human)
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100.0%; Score 250; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 250; Conservative 0; Mismatches 0;
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Bukaryota, Butheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Dases I to 3221)

Two New Single Nucleotide Polymorphisms (SNPs) in the MCP-1

Promoter in Patients with Carotid Atherosclerosis: Transcriptional Induction and New Protein Binding Sites

L Unpublished

E 2 (bases I to 3221)

S Nyquist, P.A. and Degraba, T.J.

S Nyquist, P.A. and Degraba, T.J.

Loadion, WA 22402-3300, USA

Falls Church, VA 22402-3300, USA

Location/Qualifiers
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                                                                                                         PRI 18-OCT-2000
                                                                                                                                                                                                                                                                         Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Rosl, F.
Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin structure and AP-1 composition
Oncogene 19 (29), 3235-3244 (2000)
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                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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gene="MCP-1"
                                                                                                             linear
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                  2752 TGTGGTCAGT 2761
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Ueda, A., Okuda, K., Ohno, S., Shirai, A., Igarashi, T., Matsunaga, K.,
Ueda, A., Okuda, K., Ohno, S., Ishigatsubo, Y. and Okubo, T.
Fukushima, J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Chempan B and Spl regulate transcription of the human monocyte chemoattractant protein. 1 gene
J. Immunol. 153 (5), 2052-2063 (1994)
                                                                                                                                                                                                                                                                                      Submitted (06-DEC-1993) Atsuhisa Ueda, Yokohama City University School of Medicine, First Department of Internal Medicine, 3-9 Pukuura, Kanazawa-ku, Yokohama 236, Japan (Tel:045-787-2630, Pax:045-786-3444)
Submitted (06-Dec-1993) to DDBJ by:
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     Shyy,Y.J., Li,Y.S. and Kolattukudy,P.E. Structure of human monocyte chemotactic protein gene and its
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Biochem. Biophys. Res. Commun. 169 (2), 346-351 (1990)
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Yokohama City University School of Medicine
3-9 Fukuura, Kanazawa-ku
Yokohama 236
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Phone:
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/product="small inducible cytokine A2 (monocyte chemotactic protein 1)"
join(4118. .4193,4990. .5107,5490. .5595)
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (bases 1 to 9174)

S. Rieder, M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A.,

Rajkumar, N., Toth, E.J., Yi, Q. and Nickerson, D.A.

Direct Submission

L. Submitted (106-101N-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA

To cite this work please use: SeattleSNPs, NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL:

Location/Qualifiers

L. Submitted (106-101N-101)

Location/Qualifiers

Location/Qualifiers

Lorganism=Homo sapiens"

//mol_type="genomic DNA"
//mol_type="genomic DNA"
//mol_type="genomic DNA"
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AFS19531
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                                                                                                                                                                                              7110 GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT 7169
                                                                                                                                                                                                                                                            1170 GAAGGTAAGCTGGCAGCGAGCCTGACTTTCATCTAGTTTCCTCGCTTCCTTT 7229
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                                                                                                    1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAAAATGGATTTAATGCATTGTCA
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ENGARDORA SAPLENS HONG SAPLENS BULELEGGEOMY; BULKALYOCKA; MERCALA PRIMATES; CATAININI; HOMINIGAE; HOMO.

ENGARMALIA: ELUCHERIA: PrimATES; CATAININI; HOMINIGAE; HOMO.

ENGARMALIA: Linten, L., Nusbaum, C. and Lander B.

HOMO Sapiens chromosome 17, clone hRPK.215_E.13

AL Unpublished

Unpublished

Unpublished

Los (Bases 1 to 147416)

Birren, B., Fasman, K., Linten, L., Nusbaum, C., Lander, E., Allen, N., Baiderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Anderson, M., Baker, J., Castle, A., Cenny, J., Colangelo, M., Boutwell, C., Brown, A., Castle, A., Cenny, J., Collins, S., Collymore, A., Castle, A., Cenny, J., Collins, S., Collymore, A., Castle, P., Ferreitar, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Gardyna, S., Lehoczky, J., Forrest, C., Funke, R., Gage, D., Gardyna, S., Mohalady, J., Mohala, M., Morris, W., Morrow, J., Mychaleckyj, J., Marquis, N., Morrow, J., Mychaleckyj, J., Marguis, N., Morrow, J., Mychaleckyj, J., Marguis, N., Morrow, J., Mychaleckyj, J., Pavlin, B., Peterson, K., Rilwell, J., Stojanovic, N., Stone, J., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, J., Wassiliev, H., Vo, A., Wagner, A., Wheeler, J., Whu, Y., Wyman, D., Ye, W. J., Zhoo, J. and Zody, M. Direct Submission

Direct Submission

Nahi, R., Marguis, M., Herbara, Trettitite/MIT Center for Genome Submitted Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
AC005549.1 GI:3598724
HTG.
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Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
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/replace="a"
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/replace="a"
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/replace="c"
6518
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/replace="t"
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/replace="t"
5184
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/replace="t"
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9362. .39414
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8023_8048
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                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 147416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (122-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WIGGR project 1228). The first 2Rb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
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/rpt_family="FLAM C"
complement (5441. _6051)
/rpt_family="MER81"
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Organiam="Homo sapiens"
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complement(4228. .4469)
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family="MLT1J"

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family="MIR"

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PAT 01-FEB-2002
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/codon_start=1
/db_xref="GI-487124"
/translation="MKVSAALLCLLLIAATFIPQGLAQPDAINAFVTCCYNFTNRKIS
/translation="MKVSAALLCLLLIAATFIPQGLAQPDAINAFVTCCYNFTNRKIS
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VQRLASYRRITSSKCPKEAVIFKTIVAKBICADPKQKWVQDSMDHLDKQTQTPKT"
/gone="SCYA2"
/note="monocyte chemotactic protein"
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1626 03-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2776;
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                                                                                                                                                                                                                                                                                 /number=2
1590. 1974
/gene="SCYA2"
/note="monocyte chemotactic protein intron B"
                                                                                                                                                                                             674. .1471
/gene="SCYA2"
/note="monocyte chemotactic protein intron
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/gene="SCYA2"
/note="monocyte chemotactic protein"
                                                                                                                                                                 /note="monocyte chemotactic protein"
                                                                                                                                                                                                                                        1472. .1589 |
/gene="SCYA2"
/note="monocyte chemotactic protein"
                                                                                                                                                                                                                                                                                                                                                              'note="monocyte chemotactic protein"
'note="monocyte chemotactic protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 237.4; DB 9;
Pred. No. 1.3e-65;
0; Mismatches 1;
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synthetic construct
other sequences; artificial sequences.
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                                                                                                                                                                                                                                                                                                                                    1975. .2080
/gene="SCYA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%;
Best Local Similarity 99.2%;
Matches 249; Conservative 0
                                                                                                                                         598. .673
/gene="SCYA2"
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AX346555/c
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1 (bases 1 to 2776)
Shyy Y.J., Li,Y.S. and Kolattukudy, P.E. Structure of human monocyte chemotactic protein gene and its regulation by TPA
Biochem. Biophys. Res. Commun. 169 (2), 346-351 (1990)
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/gene="SCYA2"
join(598. .673,1472. .1589,1975. .2080)
/gene="SCYA2"
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99.4%; Score 248.4; DB 9;
Best Local Similarity 99.6%; Pred. No. 5.1e-69;
Matches 249; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
598
                                                                                                                                                                                  complement (41846. .41956)
/rpt_family="purine-rich"
complement (42486. .42569)
/rpt_family="MLTII"
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Location/Qualifiers
                                                                                 /rpt_family="MBRSA"
4354. .43983
/rpt_family="LTR24"
44781. .44811
/rpt_family="AT_rich"
46184. .46296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M37719
M37719.1 GI:187447
monocyte chemotactic protein.
Homo sapiens (human)
                                                                                                                                                                    /rpt_family="MIR"
complement (47075.
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61737 TGTGGTCAGT 61728
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BOVMCPIX

3405 bp DNA linear MAM 17-JAN-1995
Bovine monocyte chemoattractant protein-1 (MCP-1) gene exons 1-3,
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MQRLMNYRRVTSSKCPKEAVIFKTILGKELCADPKQKWVQDSINYLNKKNQTPKP"
1479. .2226
/gene="MCP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wempe, F., Kuhlmann, J.K. and Scheit, K.H. Characterization of the bovine monocyte chemoattractant protein-1
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'protein id="AAA60956.1"
'db_xref="G1:624394"
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gene="MCP-1"
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|gene="MCP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        monocyte chemoattractant protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:9913"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .3405
/organism="Bos taurus"
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/gene="MCP-1"
/number=1
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2227. .2344
/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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Bos taurus
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                 Location (valifiers)
1. 5926
| organism="synthetic construct" | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forestruct | forest
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with the immune system
Patent: WO 020928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                               Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.2%; Score 160.4; DB 6; Length 5926; Best Local Similarity 77.6%; Pred. No. 1.4e-40; Matches 194; Conservative 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                      64.9%; Score 162.2; DB 6;
llarity 78.5%; Pred. No. 3.6e-41;
Conservative 0; Mismatches 53;
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Seguence 1625 from Patent W00200928.
AX346554
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                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 194; Conserv
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                      PEATURES
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(bases 1 to 279170)
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1 (Dases 1 to 279170)

1 (Dases 1 to 279170)

Allen, C., Allen, Metzker, M. Lee., Abramacon, S., Adams, C., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Barder, M., Berantseed, M., Benalmed, F., Balarian Baldwin, D., Bander, B., Barder, M., Burth, P., Barder, J., Calderon, E., Bryant, M., Buhay, C., Burth, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Ch., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Chen, J., Ch
                                                                                                                                                                                                                                                                                                   AC127645
Rattus norvegicus clone CH230-230H10, *** SEQUENCING IN PROGRESS
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                  AGGCTICTATGAIGCTACTATTCTGCAITTGAATGAGAATGGATTTAATGCATTGTCA 60
                                                                                                                                     61 gaga - accagccana acriga an accirccif acrigacif accaga accirca and
                                                                                                                                                                      DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC127645.3 GI:23195204
HTG: HTGS_PHARE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
Rattus norvegicus
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ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 14 AC127645

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ALL Submitted (08-OCT-2002) Human Genome Sequencing Center, Department Submitted (08-OCT-2002) Human Genome Sequencing Center, Department Submitted (08-OCT-2002) Human Genotics, Baylor College of Medicine, One Anylor Plaza, Houston, TX 77030, USA

ON Sep 19, 2002 this sequence version replaced gi:21953804.

ON Sep 19, 2002 this sequence eversion replaced gi:21953804.

ON Sep 19, 2002 this sequence compared assembled using Atlas and whole genome shortun sequencing reads assembled using Atlas and whole genome table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig-scaffold, assembly (a 'contigs are ordered and oriented, and separated individual sequence contigs are contest and there may be sequence by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence enly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length NOTE: Estimated insert size may differ from sequence length (see http://www.ngsc.bcm.tmc.edu/docs/Genbank draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GRWI
Center project name: GRWI
Center clone name: GRWI
Assembly program: Phrap; version 0.990329
Assembly: 146772 bases at least Q40
Consensus quality: 146740 bases at least Q20
Consensus quality: 148340 bases at least Q20
Consensus quality: 148405 bases at least Q20
Estimated insert size: 164568; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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Best Local Similarity 58.0%; Pred. No. 0.52;
Matches 69; Conservative 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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| organism="Rattus norvegicus"
| mol type="genomic DNA"
| db xxef="taxon:10116"
| clone="CH1330-230H10"
| 236659. .238546
                                                                                                                                                                                                           Rat Genome Sequencing Consortium.
Direct Submission
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240512. .241705
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/note="wgs_contig"
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Worley, K.C.
Direct Submission
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102688 TACTTTTTTTTGGATGTGTTGCTTATACTTATTTGTCGTTTGATGTTCTGAAATA 102747
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AC008692 145807 bp DNA linear PRI 18-DEC-2001
Homo sapiens chromosome 5 clone CTB-65N22, complete sequence.
AC008692
                                                                                                                                                       48567 TIGIAGITITITIAGATITIGAACAATICIGGAICAGAAAITITIGACICIGITIGGITAACA 48625
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DOB Joint Genome Institute.
DOB Joint Genome Institute.
Direct Submission
Submitsed (03-4016-1999) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 145807)
DOB Joint Genome Institute and Stanford Human Genome Center.
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                                                                           180 TTCTGCAGTTTTGGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACA 238
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DOB Joint Genome Institute and Stanford Human Genome Center.
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Best Local Similarity 53.4%; Pred. No. 1.4;
Matches 79; Conservative 0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GAATCCTTAAAATAACCCTCTTAGTTC 235
102748 TCTTCCCAAAGATTAACCCTCTTATTTC 102775
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/mol_type="genomic DNA"
/Mol_xref="texon:9606"
/chromosome="5"
/clone="CTP-65N22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC008692.6 GI:17921192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Unpublished
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AUTHORS
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JOURNAL
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SUMMARIES

Description	Adh13941 Human mon	Ade84876 Farnesvl	Adn12120 MCP1 gene	Ado03802 Human Cc1	Ado03803 Human Cc1	Abk47979 Human sma	Abl33653 Human imm	Abl33652 Human imm	Acf64398 Human MCP	Adq97310 Mouse can	Abd33157 Murine ca	Abl86846 Human ova	Aas88382 DNA encod	Aak73223 Human imm	Abk35434 Human cDN	Abk83497 Human cDN	Adq18538 Human sof	Abd20695 Human pul	Acn44442 Human gen	Adq20017 Human gof
ID	ADH13941	ADE84876	ADN12120	ADO03802	AD003803	ABK47979	ABL33653	ABL33652	ACF64398	ADQ97310	ABD33157	ABL86846	AAS88382	AAK73223	ABK35434	ABK83497	ADQ18538	ABD20695	ACN44442	ADQ20017
DB	9	10	12	12	12	9	9	Q	80	12	13	9	Ŋ	4	Q	9	12	11	11	12
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% Query Match	100.0	100.0	100.0	100.0	100.0	95.0	64.9	64.2	36.6	14.6	14.6	14.3	13.6	13.5	13.4	13.3	13.3	13.2	13.1	13.1
Score	250	250	250	250	250	237.4	162.2	160.4	91.4	36.4	36.4	35.8	34	33.8	33.6	33.2	33.2	33	32.8	32.8
Result No.		7	m	4	2	9	c 2	œ	6	c 10	c 11	c 12	13	c 14	15	16	17	18	19	20

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

Abk81833 DNA repre Abn86540 N. tabacu	Acn47169 Cotton pr	Add52904 Novel can	Abv24663 Human pro	Ada72185 Rice gene	Aad48709 Rat metab	Adj75271 Marker ge	Adj75181 Marker ge	Adr24834 Breast ca	Adj75182 Marker ge	Abx76394 Lung canc	Abx76140 Lung canc	Adn39009 Cancer/an	Abx76393 Lung canc	Abx76141 Lung canc	Adn39007 Cancer/an	Aak57161 Human imm	Aak65201 Human imm	Aak65200 Human imm	Acn45162 Human gen	Abl27938 Drosophil	Aca30151 Prokaryot	Acd05595 cDNA enco
ABK81833 ABN86540	ACN47169	ADQ52904	ABV24663	ADA72185	AAD48709	ADJ75271	ADJ75181	ADR24834	ADJ75182	ABX76394	ABX76140	ADN39009	ABX76393	ABX76141	ADN39007	AAK57161	AAK65201	AAK65200	ACN45162	ABL27938	ACA30151	ACD05595
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32.6	32	31.8	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.2	31.2	31.2	31.2	30.8	30.8	30.6
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## ALIGNMENTS

ADH13941 standard; DNA; 250 BP

RESULT 1 ADH13941

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:4. Ä Poustka Finzer P, Delius H, Disclosure; SEQ ID NO 4; 30pp; English. (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. Homo sapiens. EP1170372-A1. 09-JAN-2002. ADH13941; 

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17-JUN-2004
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                                                                                                                                                                                                                    TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
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                                                                                                                                            120
                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAATGGATTTAATGCATTGTCA
                                                                                                                                           GOGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
                                                                                                                                                             GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGAGGCCCCTTGGAATGTGGCCT
                                                                                                                                                                                          GAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTT
                                                                                                      AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 ss; cytostatic; farnesyl transferase inhibitor; gene expression;
quinolinone; leukemia; cancer.
                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                 Farnesyl transferase inhibitor modulated leukemia associated
                                                                    Length 250;
                                                                                     Indels
                                                 76 T; 0 U; 0 Other;
                                                                   Score 250; DB 6;
Pred. No. 7.9e-73;
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 95; 346pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                  Sequence 250 BP; 56 A; 60 C; 58 G;
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30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-2002; 2002WO-US034784
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                                                                    100.0%;
ilarity 100.0%;
Conservative 0
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                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chloropheny])(1-methyl-1H-imidazol-5-yl)methyl-4(3-chlorophenyl)-1-methyl-2(-(H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be
                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major histocompatibility class I; MHC-I; MHC-II; Cytostatic; EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma; gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma; parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated
                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAATAACCCTCTTAGTTCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GAAGGTAAGCTGGCAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTT
                                                                                                                                                                                                                                                                                                                     1 AGGCITCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                             <u>AGGCTTCTATGATGCTACTATTCTGATTGAGCAAATGGATTTAATGCATTGTCA</u>
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                   681;
                                                                                                                                                                                   Sequence 681 BP; 153 A; 205 C; 140 G; 183 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                 Score 250; DB 10;
Pred. No. 1.2e-72;
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                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrello IM,
                                                                                                                                          modulated in the presence of FTI
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                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 250; Conserv
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accumulation in eye

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            histocompatibility class I (MHC-1) and MHC-II antigens and which has been modified to comprise and express a gene encoding an immunomodulator and a gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma, gastric carcinoma, Burkit's lymphoma, recall lymphoma, B-cell lymphoma, parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present sequence represents a nucleotide sequence associated with the cell line
                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Cc12 promoter region used for gene knockout animal models SeqID
                                                                                                                                                                                                                                                                                                                    TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC
                                                                                                                                                                                                                                                                                                 1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
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 present invention relates to a human cell line, which lacks major
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0
                                                                                                                                                                                                                                 Length 3221;
                                                                                                                                                                                                Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                               100.0%; Score 250; DB 12; 100.0%; Pred. No. 2.5e-72;
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Matches 250; Conservative
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                                                                                                                                                                   the invention.
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                                                               This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drugs to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovasculariation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposee. This polynucleotide sequence is the human Ccl2 promoter region DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2367 GAAGGTAAGCTGGCAGCGAGCCTGACATGCTTCATCTAGTTTCCTCGCTTCCTTT
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lipofuscin accumulation, Bruch's membrane, retinal degeneration,
choroidal neovascularisation, ophthalmological, gene therapy.
                                                                                                                                                                                                                                                                                                                             100.0%; Score 250; DB 12; Length 3221; 100.0%; Pred. No. 2.5e-72; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal model; age-related macular degeneration; AMD;
                                                                                                                                                                                                                                                                                                Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Cc12 gene and enhancer region DNA SeqID 4.
                                Disclosure; SEQ ID NO 3; 64pp; English.
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Matches 250; Conservative
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WPI; 2004-400512/37.

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Disclosure; SEQ ID NO 4; 64pp; English.
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                                                                                            Best Local Similarity rov.
Matches 250; Conservative
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                  accumulation in eye.
                                                                                           Similarity
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                                                                                                                                                               New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2) gene, useful for studying the function of SCYA2, and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 gggagccgaccaaaagcrrcarccrrccrrgcragaagcccrrggaargrggccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AGGCTTCTAIGATGCTACTACTATTGCATTTGAATGAGAAATGGATTAAATGCATTGTCA
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ID ABL33653 standard; DNA; 5926
                                                                                                                                                                                                                                             Claim 1; Fig 1; 58pp; English.
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                                                                            (GENA-) GENAISSANCE PHARM INC.
                       28-AUG-2001; 2001WO-US026899.
                                                  2000US-0228496P.
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Matches 249; Conservative
                                                                                                        Anastasio AE, Finkel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human SCYA2 polypeptide
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P-PSDB; AAU77179.
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                                                     28-AUG-2000;
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07-MAR-2002
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                                                                                                                          This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Collectiont, Corlectiont, Corlectiont and/ or a Colledicient/Corlection dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Coll gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggaagccgaaaacrigaagaacriccriccriggaaagccccriggaargragcc
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                                                                                                                                                                                                                                                                                                                                                                                              1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                              Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                           Length 11793;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human small inducible cytokine A2 (SCYA2) genomic DNA.
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 250; DB 12;
100.0%; Pred. No. 4.5e-72;
Live 0; Mismatches 0;
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Gaps 1; 154 180 214 274

(first entry)

WO200218413-A2

Human immune system associated gene SEQ ID NO: 1625

(first entry)

26-MAR-2002

ABL33652;

BP.

ABL33652 standard; DNA; 5926

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1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCCATTGTCAGGG
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                                                                    antiarteriosclerotic, antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                   antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
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Human immune system associated gene SEQ ID NO: 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.9%; Score 162.2; DB 6; 78.5%; Pred. No. 6.1e-43;
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17
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                                                                                                                                                                                                                                                                                                                                                       WO200200928-A2
                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 194;
                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulaant; ophthalmological; antirheumatic; antiartic; antiarteric; antisteric; antiarter; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, nevescular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4494 AGGITITIAIGAIGTIAITAITATITICIAITIGAAIGAGIAAAAIGGAITITAAIGIAITAATIGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCCTTGGAATGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.2%; Score 160.4; DB 6; Length 5926; 77.6%; Pred. No. 2.4e-42; ive 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.6%; PL
                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-01032529
                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.6
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
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                                                                                                                                                                                                                                                                            Homo
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4734 TGTGGTTAGT 4743

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comprising: (a) a sequence comprising at least 15 contiguous nucleotides comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the of a sequence comprising variant sequences (A). Also described: (1) an array of (PN) a comprising two or more of the isolated described: (1) an array of (PN) a nonjuigual; (3) a computer-readable storage medium, where each record has a field identifying a base storage medium, where each record has a field identifying a base signal carrying data for access by an application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. ACF64025 to ACF64424 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 raciriccicciricciricciriricicaderriricaciricadadadcadaricciraa 60
                                                                                                                                      Human; detection; computer-readable storage medium; polymorphic site;
signal carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 pagrirectegerirectricerrirescagaricativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated polymucleotide (PN)
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                                                                                                                                                                                                                                                                                                                                                                                                            Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 800 BP; 185 A; 250 C; 165 G; 200 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91.4; DB 8;
Pred, No. 9.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AAATAACCCTCTTAGTTCACATCTGTGGTCAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATAACCCTCTTAGTTCACATCTGTGGTCAGT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Rienhoff HY,
                                                                                                                  Human MCP1 nucleotide sequence >MCP1_01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 74; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ97310/c
ID ADQ97310 standard; DNA; 80275 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.6%;
nilarity 98.9%;
Conservative 0
                       ACF64398 standard; DNA; 800 BP.
                                                                                                                                                                                                                                                                                                                                    07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                                                                                     07-AUG-2002; 2002WO-US025268.
                                                                                                                                                                                                                                                                                                                                                                                                                  Xu H, White R,
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-268196/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      (DNAS-) DNA SCI INC.
                                                                                                                                                                                                                                                WO2003014319-A2
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                               20-FEB-2003
                                                                                         13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                      Jones HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sclerosis
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                                                              ACF64398
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Matches
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                  ACF64398
RESULT
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66942 IdgcrdaAaacrccAdccrrrchcAccargfilccrdcAaagacafcarchirafrafr 66883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer-associated protein; CAP; cancer-associated gene; CA; gene;
                                                                                                                                                                                                                                                                    New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                              The present invention relates to cancer associated sequences (ADO97025-9098000). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AGGGAGCCGGCCAAAGGTTGAGAGCTCCTTCGTGGGAGGCCCCTTGGAATGTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67002 AadsAktrerteternAderrtagertenenengektigaerraggganggangerageee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 TGAAGGTAAGCTGGCAGCCTGACGTTTCATCTAGTTTCCTCGCTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80275 BP; 21152 A; 19490 C; 18637 G; 20855 T; 0 U; 141 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 80275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TICTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                Mouse cancer associated sequence MD08-030, SEQ ID 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 36.4; DB 12; illarity 51.2%; Pred. No. 1.7; Conservative 0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine cancer-associated (CA) gene MD07-021.
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 287; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABD33157 standard; DNA; 109559
                                                                                                                                                                            27-DEC-2002; 2002US-00330773.
                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                  22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; cancer; cytostatic
                                                                                                                                                                                                                               Malandro MS;
                                                                                                                                                                                                                                                      WPI; 2004-543781/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004058146-A2
                                                                                                   WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004
                                                                           Mus musculus.
07-OCT-2004
                                                                                                                             22-JUL-2004.
                                                                                                                                                                                                                                  Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD33157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour copypeptide encoded by a polyputcleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, cfrom the 10912 nucleotide sequences as given in ABL77023 to ABL87934, cor antigen presenting calls that express (II). (I) has cytostatic cativity. An oligonucleotide (IV) that hybridises to (S1) can be used for activity. An oligonucleotide (IV) that hybridises to (S1) can be used for cativity. An oligonucleotide (IV), detecting to (S1) can be biological semple from a patient with (IV), detecting to predetermined cutoff of serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting to a predetermined cutoff or shybridising to (IV) and comparing the amount to a predetermined cutoff or alone and thereby detecting ovarian cancer in the patient, where the computating and/or expanding T cells specific for an ovarian cutoff in design and preparation of ribozyme molecules for inhibiting cuseful in design and preparation of ribozyme molecules for inhibiting contacting the correcting T cells with (III) or (III) is useful in design and preparation of ribozyme molecules for inhibiting contacting the representation of the tumour polypeptides and proceins in tumour cells; and the process of the tumour polypeptides and proceins in tumour cells; and the contacting the representation of the contacting from a suitable library e.g., a tumour connection of the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the contacting the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AJGCTTTCATCTAGTTTCCTCGCTTCCTTTCTGCAGTTTTCGCTTCACAGAAGC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 CTGCCTGCAGGTGTGGCCCCTTTGGCCTGAACTGGGGCCTGAATTGTGGGAAGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy; forensic; food supplement, medical imaging, diagnostic, genetic disorder, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165 BP; 67 A; 37 C; 38 G; 22 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #24186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.8;
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 9824; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library using well known techniques
                                                                  Jones R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS88382 standard; cDNA; 1500 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAATCCTTAAAAATA 222
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53.7%;
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                                                                  Harlocker SL,
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Matches 73; Conservative
      (CORI-) CORIXA CORP.
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                                                                  Algate PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to cancer-associated proteins (CAP) and the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109559 BP; 31165 A; 24061 C; 22798 G; 30464 T; 0 U; 1071 Other;
                                                                                                                                                                                                                                                                                                 Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
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15-DEC-2003; 2003WO-US040081.
                                                         17-DEC-2002; 2002US-00322281.
                                                                                                                     (SAGR-) SAGRES DISCOVERY INC.
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Best Local Similarity 55.0.
Best Local Similarity
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05-SEP-2000; 2000US-0229509P.

05-SEP-2000; 2000US-0229513P.

06-SEP-2000; 2000US-0230437P.

06-SEP-2000; 2000US-023143P.

08-SEP-2000; 2000US-0231243P.

08-SEP-2000; 2000US-0231244P.

08-SEP-2000; 2000US-0231244P.

08-SEP-2000; 2000US-0231414P.

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2000US-022526P.
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27-SEP-2000;
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30-AUG-2000;
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19-MAY-2000;
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22-AUG-2000;
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                                                    09-AUG-2001
The invention relates to isolated polymucleotide (I) and polypeptide (II) squences. (I) is useful as hybridiation probes, polymerase chain caequences. (I) is useful as hybridiation probes, polymerase chain.

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymicleotides are also used in displancation as expressed sequence tags for identifying expressed contains. (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications of mutations diagnosible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in certronic format directly from WIPO at the conding activity of the conding activity from WIPO at the conding activity from WIPO at the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding activity of the conding ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035.
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                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 24186; 103pp; English.
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                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                              WPI; 2001-639362/73.
P-PSDB; ABG24195.
                                                                                                                             Liu C,
                                                                                       (HYSE-) HYSEQ INC.
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08-NOV-2000;
08-NOV-2000;
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antion acid sequences given in AAMS1921. (I) have cytostatic antion acid sequences given in AAMS1921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) to proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collynucleotides may be used to produce the secreted (I), by inserting the polynucleotides may be used to produce the secreted (I), by inserting the colline acids into a host cell and culturing the cell to express the concers and cancer immune/haematopoietic-related diseases, especially concern metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic concerns from the present invention. AAK54942 to AAK87694 captesent invention. AAK54942 to AAK87695 and AAM82169 crepresent sequences from the exemplification of the present invention
                                                                                                  human immune/hematopoletic antigen polypeptides, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I
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                                                                                                                                                                                Disclosure; SEQ ID NO 28035; 3071pp + Sequence Listing; English.
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27616 IGACTAGGGAAATIGCTIAACTGCCTTATCTGTCAATGGCCAAATTTTAAGGGTTCCTT 27557 Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; sethma; autoimmune disorder; rheumatoid arthritis; multiple selerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; infammatory disorder; crohn's disease; incision; tissue regeneration; wound healing; burn; haematopolesis; moision; myeloid cell deficiency; lymphoid cell deficiency. Human cDNA encoding secreted protein #572. ABK35434 standard; cDNA; 673 BP 06-APR-2000; 2000US-0195582P. 29-MAR-2001; 2001WO-US010224 08-MAY-2002 (first entry) WO200177288-A2 Homo sapiens. 18-OCT-2001. ABK35434; RESULT 15 ABK35434 ID ABK 

(GEMY ) GENETICS INST INC.

The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted a variety of human tissue sources and which encode novel secreted cavariety of human tissues can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The identification and isolation of full length cDNA and genomic DNA. The comparing are useful in the treatment of various immune deficiencies of polynucleotides and proteins can also be used as mutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections. Datertial infections, fungal confections, autoimmune disorders (e.g. rheumatoid arthritis, multiple colections, autoimmune thyroiditis and diabetes) and allergic reactions sclerosis, autoimmune thyroiditis and diabetes parkinson's concustodegemerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis (e.g. Crohn's disease) and tumours. They are also inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for regulating burns, incisions and ulcers. The proteins are also useful for regulating companion in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating companions and ulcers. The proteins also useful for regulating companions and ulcers. The proteins are also useful for regulating companions and ulcers. The proteins also useful for regulating companions and ulcers. The proteins also useful for regulating myeloid cell deficiencies. Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders. Resnick RJ; Sequence 673 BP; 117 A; 226 C; 168 G; 162 T; 0 U; 0 Other; Howes SH, Agostino MJ, Claim 1; Page 365; 372pp; English. Wong GG, Clark HF, Fechtel K, Gulukota K, Graham JR; WPI; 2002-179321/23

0; Gaps Query Match
Best Local Similarity 52.9%; Pred. No. 1.7;
Matches 72; Conservative 0; Mismatches 64; Indels

87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146 592 ricriicrriccrriirrricrriicacrirriirirrrrriiraricciicaaaacarc 651 532 chacchacadarandacccchadaccradacchadaccraaahrandadaahdaandan g ò

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652 AGAATTAATAACACTA 667

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68.8%; Score 172; DB 8; Length 707; 100.0%; Pred. No. 8.9e-42;

Query Match Best Local Similarity

CH230-444 CH230-48M

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Homo sapiens (human)
Homo sapiens
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (metazoa; Chordata; Catarrhini; Hominidae; Buteleostomi; Butaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 768)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Haalth, Mammalian Gene Collection (MGC)

National Institutes of Haalth, Mammalian Gene Collection (MGC)

Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Charat: Robert Strausberg, Ph.D.

Charat: Robert Strausberg, Ph.D.

Charat: ATCC

Collon Library Preparation: Life Technologies, Inc.

Collon Library Preparation: Life Technologies, Inc.

Collon Library Preparation: Life Technologies, Inc.

Collon Library Preparation: Life Technologies, Inc.

Collon Library Preparation: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:

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Syte 2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
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        Matches 172; Conservative
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

Tissue Procurement: W. Marston Linehan, Ph.D.

M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems

Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Seg primer: -dom13 fwd. ET from Amersham

High quality sequence stop: 334.

Location/Qualifiers

Location/Qualifiers

Location/Library Arrayed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI962277 161 bp mRNA linear BST 20-AUG-1999
Wq46d11.X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2474325 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
AA568299 437 bp mRNA linear BST 22-AUG-1997 nf15a05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913808, mRNA
                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 437)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.8%; Score 37; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 37; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:913808"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.____A1962277.1 GI:5754990
                                                                                                                AA568299.1 GI:2341353
                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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Unpublished (1997)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gij |473214 |qb| hlar129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ536871 481 bp DNA linear GSS 06-NOV-2000 Gm_ISb001_082_J15_R ISU Soybean BAC Library (pBeloBAC11 HindIII) Glycine max genomic clone Gm_ISb001_082_J15, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli strain XLI0-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42TNv; Purified genomic DNA from M.
musculus GS7BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    whole genome scaffolding with paired end reads from 10kb
            Mouse whole genome scaffolding with paired end reads from plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.4%; Score 36; DB 8; Length 371; Best Local Similarity 55.6%; Pred. No. 6.6; Matches 69; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: F column: 07
Seg primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0284F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:11113450
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/lab host="DH10B"
/clonellab="MCI CGAP GC6"
/note="Wetcor: pT710-Pac (Pharmacia) with a modified
/note="Wetcor: pT710-Pac (Pharmacia) with a modified
/note="Wetcor: pT710-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
secircles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonelDs
1257096-1258631, l469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
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2M0284F07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0284F07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musi
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 16).
NCI-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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14.7%; Score 36.8; DB 1; Length 161;
Best Local Similarity 54.4%; Pred. No. 2.9;
Matches 74; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2474325"
                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Unpublished (1997)
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Gaps

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REFERENCE

SOURCE

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AL (Dases & Lo. 10.).

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

The Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-rémail.inh.gov

Itssue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2791 std Error: 0.00
Seq primer: -40UP from Gibco
High quality Sequence stop: 127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="maxNa"
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/tissue type="tunor, 5 pooled (see description)"
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/clone lib="NCI CGAP_Ov23"
/note="forgan: ovary; Vector: pCMV-SPORT6; Site 1: Sall;
/note="forgan: ovary; Vector: pCMV-SPORT6; Site 1: Sall;
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Lotus corniculatus var. japonicus
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Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
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Lotus corniculatus var. japonicus DNA, clone:LjT60c08_not, genomic
survey sequence.
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Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria;
1 (bases 1 to 165)
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/clone lib="ISU Soybean BAC Library (pBeloBAC11 HindIII)"
/note="Vector: pBeloBAC11; The ISU BAC library (Marek and Shoemaker, Genome 40:420, 1997) was constructed using the HindIII site in pBeloBAC11. The library consists of HindIII site in pBeloBAC11. The library consists of approximately 40,000 clones with an average insert size of sproximately 40,000 clones with an average insert size of clone by pCR amplification of DNA pools.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://genome.cornell.edu/cgi-bin/webAce/webace?db=soybase.
Please see as an authority for the mapping/naming: Cregan P.B., T.
Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya,
T.T. VanToai, D.G. Lohnes, J. Chung, and J.E.Specht. 1999a. An
integrated genetic linkage map of the soybean genome. Crop Sci.
39: [In press]
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Contact: Shoemaker Randy C
Agronomy Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iowa State University
Ames, IA 50011-1010, USA
Tel: 515 294 1205
Fax: 515 294 2299
Email: rcsshoediastate.edu
This BAC identified by SSR Satt129. For more information, see
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/image/image.html
Insert Length, M.A. C.E. Consortium/LLNL at:
  /lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: pAGIBAC1; Site_l: HindIII; Site_2: HindIII"
                                                                                                                                                                                                            71 CAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGC 130
                                                                                                                                                                                                                                                    50 CAAATCAGAAGATGATCATACTAGCACAGATCCTCAGCCAAAACGGAGGTGAATTGTGGC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1950785 LU28 LU28 Homo Bapiens cDNA clone IMAGE:2547531 3' similar to contains element MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="INAGE:2547531"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                   170 TTATTGCTCTGTCAGCAGATAATTGAGACCAGCACCACCACCTTTAACTC 219
                                                                                                                 Length 571;
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53.7%; Pred. No. 9.8;
iive 0; Mismatches 63;
                                                                                                                 Score 35.6; DB
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
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High quality sequence stop: 145.
Location/Qualifiers
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EST.
                                                                                                                 ch 14.2%;
1 Similarity 50.6%;
86; Conservative
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Unpublished (1997)
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Oryza brachyantha

SM Oryza brachyantha

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.

Ekin, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,

Kudrna, D., Muller, C., Haffield, J., Soderlund, C. and Wing, R.

OMAP Project

L. Unpublished (2004)

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University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 621 1259
           Sato, S.

Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA ....
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA ....
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
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                                                                                                                                                                                                                                                                                          /variety="japonicus"
/db xref="taxon:34305"
/clone="lj160008_not"
/clone lib="genomic TAC library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OB_Ba0037K16.r OB_Ba Oryza brachyantha genomic clone OB_Ba0037K16.3', genomic survey sequence.
CL579550.1 GI:48537062
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 35.6; DB 9; Length 391; 60.2%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 CACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTAAAAAGATTAATGCATAAAAGTAAAAATATTAGTT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0037 row: K column: 16
Seq primer: CAC TCA TTA GGC ACC CCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://genome.arizona.edu
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         207 AGAATCCTTAAAAATA 222
                                  30 AGAATTAATAACACTA 15
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                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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/lab host="DH10B"
/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac" (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac" (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac" (Pharmacia) with a modified
was prepared from mRNA obtained from Clontech
haboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                378 bp mRNA linear EST 29-NOV-1998 gg36c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837264 3', mRNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 378)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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ilarity 53.7%;
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Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: capabb=:remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lln!gov/bbrp/image/image.html

Insert Length: 2148 Std Error: 0.00
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AI302643 396 bp mRNA linear BST 01-FBB-1999 qn48a06.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1901458 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 396)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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14.1%; Score 35.2; D.
Best Local Similarity 53.7%; Pred. No. 12;
Matches 73; Conservative 0; Mismatches
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High quality sequence stop: 375.
Location/Qualifiers
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Tue Aug

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Email: eggem@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) plate: 95 row: A column: 11
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="INRA bovine BAC"
/note="Vector: pBeloBAC11; Site 1: HindIII; Holetein bull;
INRA Bovine BAC library (Male) produced by Andre
Eggen-Genoscope sequence ID : GROAAA76AG10RM1
                                                             CR841822 641 bp DNA linear GSS 27-SEP-2004
GROAAA76AG10RM1 INRA BAC Bos taurus genomic clone INRAb_95A11, DNA
Requence, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope.

Direct Submission
Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
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                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 TGAATGAGCAAATGGATTTAATGCATTGTCAGGGAGCCGGCCAAAGCT---TGAGAGCTC 86
                                                                                                                                                                                                                                                                     Bovines, Bos.

1 (bases 1 to 641)

Sopina, Schibler, L. and Roy, A..

Bovine BAC End Sequences from the INRA bovine BAC library Unpublished

2 (bases 1 to 641)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 35; DB 9; Length 641; 54.4%; Pred. No. 16; ive 0; Mismatches 75; Indels
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/organism="Bos taurus"

/nol_type="genomic DNA"

/strain="breed: Holstein"

/db_xref="taxon:9913"

/clone="INRAb_95A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="fibroblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Animal Genetics
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Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
                                                                                                                             CR841822
CR841822.1 GI:52777910
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Matches 93; Conservative
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Bos taurus
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BH325278
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                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@miowa.edu
The following repetitive elements were found in this CDNA
seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU616089 683 bp mRNA linear EST 23-SEP-2002 UI-H-DF0-bex-i-14-0-UI.81 NCI CGAP DF0 Homo sapiens CDNA clone UI-H-DF0-bex-i-14-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Ibases 1 to 683; Primates; Catarrhini; Hominidae; Homo. NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
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TAG_SEQ=GTTAAGCGTC"
                                                                                                  BU616089.1 GI:23282297
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                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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Matches 73; Conserv
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us-09-899-276c-4.rst

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is 1 (bases 1 to 661)

Shatty, J., Shattsman, S., Tsegaye, G., Geer, K.,

Shatty, J., Shatty, J., Shatsman, S., Tsegaye, G., Geer, K.,

Shoat, S., Shetty, J., Gebregeorgis, E., Overton, L., Russell, D.,

Riggs, F., de Jong, P. and Fraser, C.M.

Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Inpublished (1999)

Contex GSSs: CH230-45113 TV

Contex Cass: CH230-45113 TV

Contex Cass CH230-45113 TV

Contex Cass CH230-45113 TV

The Institute for Genomic Research

Prax: 301 838 0208

Fax: 301 838 0208

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org

Chones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

seq primer: SP6

Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH230-45J13.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-45J13, genomic survey sequence.
BH325278
BH325278.1 GI:17255992
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /coll type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: prARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: prARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Best Local Similarity 52.4%; Pred. No. 16;
Matches 77; Conservative 0; Mismatches 70; Indels
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/mol type="genomic DNA"
/gtrain="BN/SeNHsd/MCW"
/db xref="taxon:10116"
/clone="CH230 45513"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTTCCTTTTCTGCAGTTTTCGCTTC 197
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Sequence 13209, A Sequence 2, Appli Sequence 13499, A Sequence 11845, A Sequence 11845, A Sequence 13877, A Sequence 13877, A Sequence 17614, A Sequence 17614, A Sequence 14698, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16991, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 16890, A Sequence 168
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14698, A
12245, A
12243, A
15091, A
16813, A
16813, A
16813, A
53423, A
53423, A
                                                                                                                                     August 4, 2005, 07:01:49; Search time 51.5182 Seconds (without alignments) 7940.282 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-503-922-2
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US-09-949-016-13807
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US-08-447-570-3
US-08-449-700-3
US-08-449-699A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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13.0 2943
12.6 54245
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12.5 168971
12.4 86439
12.3 601
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11.9 193169
11.8 45323
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Match Length
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Sequence 13209, Application US/09949016

Sequence 13209, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, U. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAESEQ for Windows Version 4.0

LENGTH: 198942
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Sequence 1, Appli
Sequence 12254,
                                                                                                      Sequence 16274,
Sequence 13922,
Sequence 13923,
Sequence 13924,
Sequence 13925,
Sequence 13926,
Sequence 14700,
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Sequence 13280,
Sequence 16274,
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Sequence 14702,
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                            Sequence
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US-09-148-925C-3
US-08-957-425-3
US-08-426-3431-1
US-09-423-8218-1
US-09-949-016-12254
US-09-949-016-12254
US-09-949-016-13280
US-09-949-016-13923
US-09-949-016-13923
US-09-949-016-13925
US-09-949-016-13925
US-09-949-016-13925
US-09-949-016-13925
US-09-949-016-13925
US-09-949-016-14699
US-09-949-016-14699
US-09-949-016-14700
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54.6%; Pred. No. 8.2;
7ative 0; Mismatches
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US-09-503-922-2/c
US-09-503-922-2/c
; Sequence 2, Application US/09503922
; Patent No. 6410706
; GENERAL INFORMATION:
; APPLICANT: PAI, HYUN-Sook
; APPLICANT: LIU, Jang-Ryol
; APPLICANT: CHO, Hye-Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(198942)
; OTHER INFORMATION: n = A,T,C or US-09-949-016-13209
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Best Local Similarity 54.6
Matches 65; Conservative
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17415
17415
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139952
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LOCATION: (1)...(19894;
                                       RESULT 1
US-09-949-016-13209/c
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ORGANISM: Human
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TYPE: DNA
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US-09-949-016-13499
i Sequence 13499, Application US/05949016
sequence 13499, Application US/05949016
sequence 13499, Application US/05949016
sequence 13499, Application US/05949016
center No. 6812339
resultant inventation: Volver al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTE EN ENTIRE OF SEC OF WINDOWS Version 4.0
SEQ ID NO 13499
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APPLICANT: KIM, Youn-Sung
TITLE OF INVENTION: A NOVEL CHITIN-BINDING RECEPTOR KINASE AND THE GENE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8eg
CURRENT APPLICATION UNMBER: US/09/503,922
CURRENT FILLING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                          88 TICCIGGCIGGGAGGCCCCTIGGAATGTGGCCTGAAGGIAAGCTGGCAGCGAGCTGACA
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12.6%; Score 31.6; D
Best Local Similarity 50.7%; Pred. No. 8.6;
Matches 76; Conservative 0; Mismatches
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54.1%;
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; ORGANISM: Nicotiana tabacum
US-09-503-922-2
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Best Local Similarity 54.11
Matches 66; Conservative
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ORGANISM: Human
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RESULT 5
US-09-949-016-13807

J Sequence 13807, Application US/09949016

J Sequence 13807, Application US/09949016

GENERAL INFORMATION:

J TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,758

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13807

LENGTH: 168971
           Sequence 58722, Application US/09949016

Fatent No. 681233

Patent No. 681234

FAPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1107

CURRENT PLILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF WINDOWS VERSION 4.0

SEQ ID NO 58722

LENGTHARE: PRESENCE OF WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 CCCAAGGCCAATGTGAAAAGGACATTTCACTGAGGACATGATGGGGTTGCCTTGTTTT 364
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0
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Pred. No. 0.68;
1; Mismatches 57; Indels
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Best Local Similarity 52.8%;
Matches 65; Conservative 1
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Best Local Similarity
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US-09-949-016-58722
RESULT 4
US-09-949-016-58722
; Sequence 58722, Ax
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RESULT 8
US-09-949-016-177614/c
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                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                               US-09-949-016-16990
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US-09-949-016-13877
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                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
FRICE REPEATOR TELLING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                             93014 Trrchadargradacadacadacacanaacadadacrecrecrecrerrarcradarac 93073
                                                                                                                             93074 CTACCTAAGCAGGAAGATGGCTGCCAGCTGGGCTTGCCGCCCATGCTCTTGTTCCA 93133
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                               106 CTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCC
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Pred. No. 19;
0; Mismatches 40; Indels
 Mismatches 103; Indels
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Patent No. 6812339
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ilarity 57.9%;
Conservative
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Best Local Similarity
.....hes 55; Conserve
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Sequence 177614, Application US/09949016
| Sequence 177614, Application US/09949016
| Patent No. 681233
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TILLE REPERENCE: CL001307
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
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Sequence 13877, Application US/09949016

Sequence 13877, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION WHERE: 2009-94-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20
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Best Local Similarity 57.9%; Pred. No. 19;
Matches 55; Conservative 0; Mismatches 4
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56.0%; Pred. No. 1.1;
tive 1; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 16990
LENGTH: 86440
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177614
LENGTH: 601
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Best Local Similarity 56.0°
Matches 56; Conservative
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Query Match
Best Local Similarity
Matches 65; Conserv
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ORGANISM: Human
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US-09-949-016-17188
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US-09-949-016-58723
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) Sequence 14449, Application US/09949016

) Patent No. 6812339

) GENERAL INFORMATION:

APPLICANT: VEXTER. VEXTER.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFUTARE: PastSEQ for Windows Version 4.0

LENGTH: 34088
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Best Local Similarity 57.1%; Pred. No. 37;
Matches 56; Conservative 0; Mismatches 42;
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12.2%; Score 30.6; DE
Best Local Similarity 52.8%; Pred. No. 15;
Matches 66; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRAELED for Windows Version 4.0
SEQ ID NO 13877
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| LCCATION: (1)...(202111)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877
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US-09-949-016-58723
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US-09-949-016-14449
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                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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Sequence 1718b. Application US/09949016

Sequence 1718b. Application US/09949016

Sequence 1718b. Application US/09949016

Sequence 1718b. Application US/09949016

SERERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE REPERBUCE: CLOOO-0-0-14

PRIOR FILING DATE: 2000-0-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-0-0-03

PRIOR PILING DATE: 2000-0-0-03

PRIOR PILING DATE: 2000-0-0-0-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREATSEQ for Windows Version 4.0

SEQ ID NO 17188

LENGTH: 31797
          Sequence 58723, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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al Similarity 53.9%; Pred. No. 20;
62; Conservative 0; Mismatches
Application US/09949016
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Best Local Similarity
Matches 62; Conserv
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, OTHER INFORMATION: n = A, T, C or G US-09-949-016-14698
                                                                   Query Match
Best Local Similarity 61.5%;
Matches 48; Conservative
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Best Local Similarity 61.5%;
Matches 48; Conservative
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOTHARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 13444
MANDER OF SEG ID NOS: 20707
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL WINDOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111696 CCCAAGGCCAATGTGAAAAGGACATTTCACTGAGGACATGATGGGGGTTGCCTTGTTTT 111755
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189 TITCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATCTGT
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Pred. No. 56;
0; Mismatches
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SOFTWARE: PSSESEQ for Windows Version 4.0
SEQ ID NO 14698
LENGTH: 18895
                                                                                                                                                     Sequence 13444, Application US/09949016
Patent No. 6812339
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Best Local Similarity 52.8%;
Matches 65; Conservative
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LOCATION: (1)...(18895)
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ORGANISM: Human
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RESULT 15

19-09-049-016-12245/c

sequence 12245, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRESENCE: CLOOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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  DB 4;
17;
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51;
Score 30; DB 4
Pred. No. 17;
0; Mismatches
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Pred. No.
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12245
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 4, 2005, 08:04:16 ; Search time 445.951 Seconds

Run on:

(without alignments) 3633.986 Million cell updates/sec

US-09-899-276C-4 Title: Perfect score:

1 aggettetatgatgetaeta......agtteaeatetgtggteagt 25( Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

7297361 segs, 3241162794 residues Searched:

Total number of hits satisfying chosen parameters:

14594722

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

| cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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| cgn2\_6/ptodata/1/pu 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		quence 4, Appli	equence 95, Appl	equence 3, Appli	equence 4, Appli	equence 2, Appli	equence 1626, Ap	Sequence 1625, Ap
			Desc		Sec	Š	Š	ഗ്	Š	ഗ്	Š
SUMMARIES			ID	***********************	US-09-899-276-4	US-10-283-975A-95	US-10-685-705-3	US-10-685-705-4	: US-10-833-656-2	. US-10-311-455-1626	5 15 US-10-311-455-1625
			DB	1	0	19	19	19	22	15	12
			Match Length DB ID		250	681	3221	11793	2776	5926	5926
	de	Query	Match		100.0	100.0	100.0	100.0	95.0	64.9	64.2
			Score		250	250	250	250	237.4	162.2	160.4
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3 US-10-027-632-121412 VS-10-027-632-121412 9 US-10-322-281-137 US-09-867-701-9824 US-09-822-849A-572 US-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154 VS-10-027-632-45154	0 US-09-940-227-19-09-0-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-19-09-	7 US-10-027-632-136 7 US-10-027-632-136 3 US-10-087-192-197 3 US-10-719-993-711 1 US-10-719-993-711 1 US-10-719-993-711 3 US-10-027-632-221 7 US-10-027-632-203 7 US-10-027-632-203 7 US-10-282-122A-18 8 US-10-243-552-194 8 US-10-243-552-194 8 US-10-243-552-194 8 US-10-243-552-194 9 US-10-195-193-673-67 4 US-10-75-523-96 9 US-10-767-701-109
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## ALIGNMENTS

APPLICANT: Roel, Frank
APPLICANT: Soco, Ubaldo
APPLICANT: Soco, Ubaldo
APPLICANT: Soco, Ubaldo
APPLICANT: Cov, Johannea
APPLICANT: Patrick
APPLICANT: Delius, Hajo
APPLICANT: Delius, Annemarie
APPLICANT: Zur Hausen, Harald
APPLICANT: Patrick, Annemarie
APPLICANT: Patrick, Annemarie
APPLICANT: Patrick, Andrea
TITLE OF INVENTION: No. US20020106355A1e1 Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: No. US20020106355A1e1
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT APPLICATION NUMBER: ED 00 114 560.6
PRIOR APPLICATION NUMBER: ED 00 114 560.6
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0 ; Sequence 4, Application US/09899276 ; Patent No. US20020106355A1 ORGANISM: Homo sapiens GENERAL INFORMATION: US-09-899-276-4 TYPE: DNA SEQ ID NO 4

Gaps ;; 0 Query Match 100.0%; Score 250; DB 9; Length 250; Best Local Similarity 100.0%; Pred. No. 1e-72; Matches 250; Conservative 0; Mismatches 0; Indels

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RESULT 4
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                                                                                              GAAGGIAAGCIGGCAGCCIGACAIGCITICAICIAGIITCCICGCIICCIIT 180
                                                                                                                                                       TCTGCAGITTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
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; Sequence 95, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
APPLICANT: Ortho-clinical Diagnostics, Inc.
APPLICANT: Ortho-clinical Diagnostics, Inc.
APPLICANT: Ortho-clinical Diagnostics, Inc.
APPLICANT: ORTHORNER: US/10/283,975A
CURRENT ELING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; RIOR FILING DATE: 2001-10-30
; SEQUENCE: PARTICATION NUMBER: 60/341,012
; RIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SEQUENCE: PARTICATION NUMBER: 60/341,012
; SEQ ID NO 95
; LENGTH: 681
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100.0%; Score 250; DB 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 250; Conservative 0; Mismatches 0;
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Best Local Similarity
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US-10-283-975A-95
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Sequence 4, Application US/10685705;
Sequence 4, Application US/10685705;
Publication No. US20040177387A1;
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: UNIVERSITY OF Mibati
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular;
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415;
CURRENT APPLICATION NUMBER: 050422,096
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 4
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                 Sequence 3, Application US/10685705; Sequence 3, Application US/10685705; Sequence 3, Application US. US2004017387A1
; Publication No. US2004017387A1
; GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular; TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415; TURENT APPLICATION NUMBER: 05/10/685,705
CURRENT FILING DATE: 2003-10-16
PRIOR FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
; SEQ ID NOS: 10
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2427 TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 2486
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Best Local Similarity 100.0%; Pred. No. 5.1e-72;
Matches 250; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 250; DB 19;
Best Local Similarity 100.0%; Pred. No. 2.9e-72;
Matches 250; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-10-685-705-4
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; ORGANISM: Homo sapiens
US-10-685-705-3
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RESULT 3
US-10-685-705-3
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DETERBRENCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: Cyclsine methylation
TITLE OF INVENTION: Cyclsine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICANTON NUMBER: US/10/311,455
FRIOR APPLICATION NUMBER: DCT/EPO1/07537
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1626
LENGTH: 5926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                           ; Sequence 1626, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                          275 CTGTGGTCAGT 285
                                                                   240 CIGIGGICAGI 250
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US-10-311-455-1626/c
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; Sequence 2, Application US/10833656
; Publication No. US20050148507A1
; GENERAL INFORMATION:
; APPLICANT: Wand1, Robert
; APPLICANT: Neclina, Roman
; APPLICANT: Lenter, Martin
; APPLICANT: Lenter, Martin
; APPLICANT: Lenter, Martin
; APPLICANT: Lenter, Martin
; APPLICANT: Lenter, Martin
; APPLICANT: Lenter, Martin
; APPLICANT: Case 1/1492
; TITLE OF INVENTION: Chemotactic factor
; TITLE OF INVENTION: Chemotactic factor
; TITLE OF INVENTION: Marbin (Fig. 1492)
; CURRENT FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENTER: PatentIn version 3.1
; SEQ ID NO 2
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                                                                                                              7110 GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
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NAME/KEY: misc feature
LOCATION: (2585). (2585)
OTHER INFORMATION: n = c, a, t or
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LOCATION: (2582)..(2582)
OTHER INFORMATION: n = c, a
FEATURE:
LOCATION: (2583)..(2583)
OTHER INFORMATION: n = c, a
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ORGANISM: Homo sapiens
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TYPE: DNA
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| Publication No. US20020198371A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| PRIOR FILING DATE: 2000-07-12
| PRIOR FILING DATE: 2000-04-20
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-08-08-09
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64.2%; Score 160.4; DB 15; Length 5926;
Best Local Similarity 77.6%; Pred. No. 2.7e-42;
Matches 194; Conservative 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1625
PRIOR APPLICATION NUMBER: 2002-12-16
PRIOR PLING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
LENGTH: 5926
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121412
LENCTH: 934
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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US-10-027-632-121412
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; Sequence 137, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
    APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; CURRENT FILING DATE: 2002-12-17
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SEQ ID NO 137
; LENGTH: 109559
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Length 934;
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                                                                   1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTA
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                                0; Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                              ; Sequence 121412, Application US/10027632; publication No. US20030204075A9; GENERAL INFORMATION:
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LOCATION: (1)...(109559)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100..
Local 49; Conservative
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Sequence 1357, Application US/10723860

Publication No. US20040253606A1

Publication No. US20040253606A1

Publication No. US20040253606A1

APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Ginsburg, Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26

PRIOR FILING DATE: 2002-11-26
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                   APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REPERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 572
LENGTH: 673
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; Pred. No. 30;
0; Mismatches
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13.4%; Score 33.6; DE
Local Similarity 52.9%; Pred. No. 1.9;
188 72; Conservative 0; Mismatches
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SOFTWARE: Patentin version 3.2
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Best Local Similarity 57.00
مام 259; Conservative
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US-09-822-849A-572
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US-10-723-860-1357
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Fatent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Adlacker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: UNMERR: 120121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: PastSEQ for Windows Version 4.0
ISBQ ID NO 9824
LIENGTH. 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.3%; Score 35.8; DB 9; Length 165; Best Local Similarity 53.7%; Pred. No. 0.2; Matches 73; Conservative 0; Mismatches 63; Indels
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                                                                                              Indels
                                                                                                                                                                                                                                                                                                                           156 TCTAGTTTCCTCGCTTCCTTTCTGCAGTTTTCGCTTC 197
                                           Score 36.4; DB 19;
Pred. No. 1.9;
0; Mismatches 71;
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Sequence 572, Application US/09822849A
Patent No. US2002005170A1;
GENERAL INFORMATION:
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Footsino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(165)
OTHER INFORMATION: n = A, T, C or
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ilarity 55.6%;
Conservative
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LOCATION: (1)...(165)
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                                      Query Match
Best Local Similarity
Matches 90; Conserv
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-09-867-701-9824/c
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US-10-322-281-137
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218133 ccaeccrcaaaacrcrarearcaeaeecacrreeraeecr 218174
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US-10-027-632-45154
; Sequence 45154, Application US/10027632
; Publication No. US20020198371A1
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i Sequence 45154, Application US/10027632

j Publication No. US20030204075A9

i GENERAL INFORMATION:
   APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
   TITLE OF INVENTION: Polymorphisms in the Human Genome
   TITLE OF INVENTION: Polymorphisms in the Human Genome
   FILE REFERENCE: 108827.129

   CURRENT APPLICATION NUMBER: US/10/27,632

   CURRENT APPLICATION NUMBER: US/00/6718,006

   PRIOR FILING DATE: 2000-07-12

   PRIOR FILING DATE: 2000-07-12

   PRIOR FILING DATE: 2000-03-29

   PRIOR PELING DATE: 2000-03-29

   PRIOR PELING DATE: 2000-03-29

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   PRIOR FILING DATE: 2000-03-24

   PRIOR FILING DATE: 1999-11-23

   PRIOR FILING DATE: 1999-11-23

   PRIOR FILING DATE: US 60/156,358
THILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REPERRICE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR APPLICATION NUMBER: US 60/18,676
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 12000-03-29
PRIOR PILING DATE: 12000-03-29
PRIOR PILING DATE: 1909-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
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PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FASTSEQ for Windows Version 4.0
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Pred. No. 3.2;
1; Mismatches
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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48.4%;
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                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-45154
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AC136446 Homo sapi
AC1007533 Homo sapi
AC130814 Homo sapi
AC092594 Homo sapi
AC099934 Mus muscu
BX649242 Zebrafish
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Regulatory sequences of the human mcp-1 gene
Patent: EP 1170372-A 5 09-JAN-2002;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS (DE)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CR545242
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AL1357150
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D26087 Human gene
AF515531 Homo sapi
AC005549 Homo sapi
XY357296 Homo sapi
XY85739 Homo sapien
AC021520 Homo sapien
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12055.236 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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Jeass 1 to 3227)

Ueda,A., Okuda,K., Ohno,S., Shirai,A., Igarashi,T., Matsunaga,K.,

Fukushima,J., Kawamoto,S., Ishigatsubo,Y. and Okubo,T.

NF-kapap B and Spl regulate transcription of the human monocyte
chemoattractant protein-1 gene
J. Immunol. 153 (5), 2052-2063 (1994)
                                                   241 TCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT 300
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-DEC-1993) Atsuhisa Ueda, Yokohama City University School of Medicine, First Department of Internal Medicine; 3-9 Fukuura, Kanazawa-ku, Yokohama 236, Japan (Tel:045-787-2630, Fax:045-786-3444)
                                                                                                                                                                                                                                                                                                                                     1 (sites)
Rollins,B.J., Stier,P., Ernst,T. and Wong,G.G.
The human homolog of the JB gene encodes a monocyte secretory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          First Department of Internal Medicine Yokohama City University School of Medicine 3-9 Fukura, Kanazawa-ku Yokohama 236
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Homo sapiens (human)
Homo sapiens
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Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Rajedar, M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., Rajkumar, N., Toth, B.J., Yi,Q. and Nickerson, D.A.

Direct Submission

Submission

Sciences, University of Washington, Submitted (06-JUN-2002) Genome Sciences, University of Washington, Submission

To cite this work please use: SeattleSNPS. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: Logangs, Washington, edu).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9174 bp DNA linear PRI 09-JUL-2002 Homo sapiens small inducible cytokine A2 (monocyte chemotactic protein 1) (SCYA2) gene, complete cds. AF519531
                                                                                                                                                                                                                                                                                                                                                                                                                                2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1892 AACTGAGGAATGAAGGTTACGAATTCCGGAAATACTCCTCCACGGTTACTCATG 1951
                                                                                                                                                                                                                                                                    241 TCCTTGGAAATTAAGAAGGAAGCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGGAC
                                                                                                                                                                                                                                                                                                                              61 TIBACATGCCTCAAGTACTCCTATCATATTGTAAGACACAACAGTTCACTGAAATGAAT
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/number=1
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                                                                                                                                                                                                           0; Indels
                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 300; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/replace="g"
604
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/replace="g"
305
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gion	variation 1051 /frequent replace variation 1054 /frequent/replace variation 1072	variation / replace variation 1280 / replace variation 1537 / replace variation 1548 / replace / replace / replace / replace / replace	/replace variation 1563 1563 /reques variation 1707 /reques /reques /replace repeat_region 1118.	variation   /rpt_type=di.  variation   /replace="c" variation   /replace="t" variation   /replace="g" variation   /replace="g" variation   /replace="g" variation   /replace="g" variation   /replace="a" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" variation   /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t" /replace="t"

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Ye,W.J., Zhao,J. and Zody,M.

Direct Submission

Submitted (27-AuG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa barren, B., Pasaman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Coole,P., Corliss,D., Depayre,E., Devon,K., Dewar,K., Cooke,P., Coorliss,D., Depayre,E., Devon,K., Dewar,K., Gago,D., Gardyna,S., Geraigery,K., Grant,G., Hagos,B., Hadford,A., Herena,L., Horton,L., Howland,J.C., Grant,G., Jacotot,L., Jones,C., Kann,L., Raratas,A., Lehozky,J., Macdonald,P., Marquis,N., Morrow,J., Mychaleckyj,J., Nallor,J., Nolla,M., Morris,W., Morrow,J., Mychaleckyj,J., Nallor,J., Niloff,M., O'Connor,T., O'Donnell,P., Ravige-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C., Subrasian,A., Teefaye,S., Tichovolsky,N., Torruella-Miller,I., Vassiliev,H., Vo.A., Wagner,A., Wheeler,J., Wu,Y., Wu,Y., Wyman,D., Ye,W.J., Zhao,J. and Zody,M.

Direct Submission

Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project 1228). The first 2Xb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mol_type="genomic DNA"
/db zref="taxon:9606"
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17pt family="MRR5A"

/rpt family="MRR5A"

/rpt family="MRR5A"

/rpt family="MRR5A"

/rpt family="MRR"

complement (1428. 4469)
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/rpt_family="BUR1"
490. .695
/rpt_family="LIME2"
1291. .1390
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                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC005549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2757 AAGGAGGAGCAGTGGGCTAGGAGAATCGAGAGTCAGAATTTTAAACTCAGCCCAGCCA 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2877 ICTAAGGICTTIGGGITTTIAICAGIGIGCTICTGIAGTTICTGAGGAAAICTAAGGGAC 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2997 TCCCTTGGAAATTAAGAAGGAAGGAGGAGAATAGCTGCCATAACCAGGGATGAACTTCT 3056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TCCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT 300
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
1 (bases 1 to 147416)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.215_E_13
Unpublished
2 (bases 1 to 147416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAGGAGGAGGCAGTGGGCTAGGAGAATCGAGAGTCAGAATTTTAAACTCAGCCCAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 298.4; DB 9;
Pred. No. 1.4e-82;
0; Mismatches 1;
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8272. .8734

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8597
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8775
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Best Local Similarity 99.7
Matches 299; Conservative
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                                                                                                            repeat_region
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| 12501. . 12981
| 7pt family="L2"
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62598 AACTGAGGAATGAAGTCAGGCTTTCCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 62539
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Homo sapiens MCP1 (MCP1) gene, promoter region and partial cds.
AY357296
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2 (bases 1 to 3221)
Nyquist.P.A. and Degraba,T.J.
Direct Submission
Submitted (31-JUL-2003) Medicine, Inova Fairfax, 3300 Gallows Road, Falls Church, VA 22402-3300, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TCCCTTGGAAATTAAGAAGGCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT 300
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( bases 1 to 3221)

Nyquist, P.A. and Degraba, T.J.

Two New Single Nucleotide Polymorphisms (SNPs) in the MCP-1

Promoter in Patients with Carotid Atherosclerosis: Transcriptional Induction and New Protein Binding Sites
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99.5%; Score 298.4; DB 9; Length
Best Local Similarity 99.7%; Pred. No. 1.6e-82;
Matches 299; Conservative 0; Mismatches 1; Indels
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Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
                                                                                                         Delius, H., Patzelt, A., Coy, J.F., Poustka, A.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                               Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., zur Hausen, H. and Roal, F. Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in non-tumorigenic HPV 18 positive cells: the role of structure and AP-1 composition Oncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(7610 . 7685,8468 . .8585,8968 . .9073)
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codon_start=1
            MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
Homo sapiens
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join(<7550. .7685,8468. .8585,8968.

/gene="MCP-1"

/gene="MCP-1"
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| Ab Aref="texon:9606" |
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Homo sapiens MCP-1 gene and enhancer region.
Y18933
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 73806)
                              6309 TTAACATGCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence submissions@genome.wi.mit.edu Project Information Center project name: L5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens chromosome 17, clone RP11-329H16 Unpublished
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Web site: http://www-seq.wi.mit.edu
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50138 50078 3812 ö 3813 TTTAAGGTTTTTTGGTTTTTTAGTGTGTTTTTTGTAGTTTTTAAGGAAATTTAAGGTAT 3872 PAT 01-FEB-2002 300 240 3693 AAGGAGGAGGTAGGGTTAGGAGAATTCAGAGAGATTAGATTTAAATTTAGTTTAGTTTAGTTTA 61 TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTTCTGAGGAAATCTAAGGCAC TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 50077 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG TCCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT 1. :5926 /organism="synthetic construct" /mol type="unassigned DNA" /db xref="taxon:32630" /note="chemically treated genomic DNA (Homo sapiens)" 1 AAGGAGGAGGCAGTGGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCA 181 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTTCTGTAGTTTCTGAGGAAATCTAAGGCAC AAGGAGGAGGCAGTGGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCA AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG Gaps Gaps ; 0 ;; Olek, A., Piepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers Length 73806; Score 204; DB 6; Length 5926; Pred. No. 6.9e-53; 0; Mismatches 60; Indels Indels linear Score 284.8; DB 2; Pred. No. 2.9e-78; 0; Mismatches 2; AX346554 5926 bp DNA Sequence 1625 from Patent WO0200928. AX346554 other sequences; artificial sequences AX346554.1 GI:18494440 Query Match
Best Local Similarity 80.0%;
Matches 240; Conservative 94.9%; 99.0%; synthetic construct synthetic construct Query Match
Best Local Similarity 99.0
Matches 297; Conservative 3873 121 181 241 121 61 50196 AX346554 LOCUS DEFINITION source ORGANISM ACCESSION VERSION TITLE JOURNAL AUTHORS KEYWORDS SOURCE REFERENCE FEATURES RESULT ORIGIN g 셤 ò 셤 ò 셤 ઠ 셤 ò g à 셤 ò 셤 ò ਨੇ 셤 ò à

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join(1403. .1478,2227. .2344,2695. .2800)
/gene="MCP-1"
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1479. .2226
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/mimho--.
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Mus musculus Balb/c macrophage chemoattractant protein-1 (mcp-1)
gene, 5' flanking region.
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chemokine; mcp-1; macrophage chemoattractant protein-1.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87.6; DB 4;
Pred. No. 2.7e-16;
0; Mismatches 69;
mol_type="genomic DNA'
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                                                                                                       /note="putative"
1342. .1478
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3202. .3207
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/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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Best Local Similarity 67.9%;
Matches 152; Conservative (
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Bovine monocyte chemoattractant protein-1 (MCP-1) gene exons 1-3,
Complete cds.
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Wempe, F., Kuhlmann, J.K. and Scheit, K.H.
Characterization of the bovine monocyte chemoattractant protein-1
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

    .5926
    /organism="synthetic construct"
    /mol type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="chemically treated genomic DNA (Homo sapiens)"

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Blocchem. Biophys. Res. Commun. 202 (3), 1272-1279 (1994)
94338337
                                                                                                                                                                                                               Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with the immune system Patent: WO 020928-A 1626 03-JAN-2002; Bpigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5926;
                                                     linear
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64.8%; Score 194.4; DB 6;
Best Local Similarity 78.0%; Pred. No. 7.2e-50;
Matches 234; Conservative 0; Mismatches 66;
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                                        5926 bp DNA Sequence 1626 from Patent W00200928. AX346555.
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synthetic construct
other sequences; artificial sequences.
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monocyte chemoattractant protein-1.
Bos taurus (cow)

    .3405
    /organism="Bos taurus"

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Bukaryora, thereases,

Mus musculus

Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryora, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 160869)

I (bases 1 to 160869)

Sis Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,

Dederich, D., Thomas, S., Okwhoun, G., Bonnin, D., Brooks, A., Brown, J.,

Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,

Buhay, C., Davis, C., Delgado, O., Ding, Y., Ougan-Rocha, S.,

Fernandez, C., Perraguto, D., Forcum-Tansey, J., Gill, R.,

Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,

Hosak, H., Hou, X., Huber, J., Jackson, L., Jaz, Y., Kelly, S.,

Kovar, C., Liu, J., Liu, W., Lollseged, H., Lozado, R.J., Martin, R.,

Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
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), *** SEQUENCING IN PROGRESS ***, 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1723 TCTAAGGGCTTTCAGATTTTATGGCTTTGATCACACTGTTTGTGAAGAAATCTAAACCTG 1782
                 Rollins, B.J., Morrison, B.D. and Stiles, C.D.
Cloning and expression of JE, a gene inducible by platelet-derived
growth factor and whose product has cytokine-like properties
Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3738-3742 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TIAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAAGGTCTTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                    3 (bases 1 to 2788)
Abberta, 7.A.
Direct Submission
Submitted (20-JUL-1994) John A. Alberta, Cellular and Molecular
Biology, Dana Farber Cancer Institute and Harvard Medical School,
44 Binney St., Boston, MA 02115, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="mcp-1"
/product="macrophage chemoattractant protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 2788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.7%; Score 68; DB 10, 59.7%; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_line="Balb/c 3T3 A31"
/cell_type="fibroblast"
2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                      1. .2788
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="Balb/c"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus clone RP23-433DB, unoxdered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="JEJCI-50"
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                                                                                                                                                                                                                                                                                                                   Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetice, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11079355.
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B., Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S. Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R.
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                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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2 (bases 1 to 180944)
DOB Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 18944)
DOB Joint Genome Institute.
Sequencing of Mouse
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
Consensus quality: 143665 bases at least Q40
Consensus quality: 160562 bases at least Q20
Consensus quality: 164105 bases at least Q20
Consensus quality: 164105 bases at least Q20
Estimated insert size: 194000; pulse field gel estimation
Estimated insert size: 194000; pulse field gel estimation
Quality coverage: 6.92 in Q20 bases; pulse field gel estimation
Quality coverage: 7.62 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Center clone name: RPCI-23_92G22
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Mus musculus clone RP23-92G22, WORKING DRAFT SEQUENCE, 48 unordered
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Mus musculus (house mouse)
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Direct Submission

Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 222121)

Burdan, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chargaro, B., Erown, A., Camarata, J., Campopiano, A., Chang, J., Chargaro, B., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Diaz, J.S., Dodge, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Ciaham, L., Grand-Pierre, N., Gardyna, S., Gands, B., Horton, L., Hulme, W., 11iev, I., Johnson, R., Jones, C., Kamat, A., Kartasa, A., Kells, C., Lakocque, K., Landarares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacDand, P., Mayor, J., Marquis, N., Merkens, C., MacCanlad, P., McKernan, K., Meldrim, J., Menga, J., McKernan, K., Meldrim, J., Meldrim, J., Meldrim, J., Meldrim, J., Rosman, C., Rette, R., Rieback, M., Santos, R., Schugback, R., Strauss, N., Subramanian, A., Taravers, M., Subramanian, A., Taravers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Tr
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130636 AAGGATGCTACAGAGGAAGGAAATCAAGATACCTGAGTGGAAGACTCCGCTCAGCCA 130695
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Birren,B.; Linton,L.; Nusbaum,C. and Lander,E.
Mus musculus chromosome 11, clone RP23-328G11
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AC012294/c
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Query Match 22.7%; Score 68; DB 2; Length 180944; Best Local Similarity 59.7%; Pred. No. 4.6e-10; Matches 135; Conservative 0; Mismatches 85; Indels 6;

/clone="RP23-92G22" /clone\_lib="RPCI mouse BAC library 23"

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22.7%; Score 68; DB 10; Length 222121;
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complement (30238, .30446)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt family="(CAAA)n"
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rpt family="B1 MM"
complement(19335. .19554)
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4235. .24267
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complement(28973.
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S Birren, 340 Lonaines Street, Cambridge, MA 02141, USA
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L.,
Boukhgalter, B., Erna, N., Bastien, V., Bloom, T., Boguelavkiy, L.,
Boukhgalter, B., Tonem, A., Colangelo, M., Colling, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Graham, L., Grand-Pierre, N.,
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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MacLenn, C., Macdonald, P., Major, Y., Martues, C., Micol, R.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Martues, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
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Raymond, C., Retta, R., Rieback, M., Stange-Thomann, N., Schauback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Viel, R., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Yoo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAZ 25, 2002 This sequence version replaced gi:19683729. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-23 Female Mouse BAC"
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complement(7561. .7875)

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Center clone name: 32
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                   REFERENCE
AUTHORS
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Gaps 9

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12896 chackkakaranakacakaranthhar----kakakarachkakahakan 12843
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                                                       1 AAGGAGGAGGCAGTGGGCTAGGAGATCGAGAGTCAGAATTTTAAACTCAGCCCAGCCA
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0; Mismatches
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            Matches 135; Conservative
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Direct Submission

Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (04-APR-2002) Wellcome requests: clonerequest@sanger.ac.uk

Now 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version replaced gi:17065774.

On Nov 30, 2001 this sequence version and note that the together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone, as we submit sequences with conty a small overlap as described above.

Only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality data (i.e., phred quality >= chamistry or covered by high quality as second or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the second or more databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em:, EMBL; Sw:, http://www.sanner.ar.uk/Doriects/C elecans/wormene RP23-35061 is
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Mouse DNA sequence from clone RP23-350G1 on chromosome 11, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICTAAGGICTITIGGGITTITIATCAGIGCTICTGTAGTTTTCTGAGGAAATCTAAGGGAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                   61 TIPACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCC 226
                                                                                     85; Indels
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Pred. No. 4.6e-10;
                                                   Pred. No. 4.6e-10;
0; Mismatches 85
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="l1"
/clone="RP23-35091"
/clone_lib="RPCI-23"
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Rodentia;
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AL626807.7 GI:17221258
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                                                               59.78;
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Eukaryota; Metazoa;
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                                                                                                      Matches 135; Conservative
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AL626807/c
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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RESULT 1
                                                                                                        August 3, 2005, 15:09:47; Search time 198.826 Seconds (without alignments) 8932.047 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             4390206 segs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adhi3942 Human mon	Adn12120 MCP1 gene	Ado03802 Human Cc	Ado03803 Human Cc	Abl33652 Human imm	Abl33653 Human imm	Acn44486 Human gen	Abk52382 DNA encod	Aas34422 Human DNA	Adn41808 Novel hum	07 Continuation (8 of	07 Continuation (8 o	_07 Continuation (8 o	07 Continuation (8 of	Aas70462 DNA encod	Aas72056 DNA encod	Aca30296 Prokaryot	Acn44070 Human gen	Aas61419 Human gen	Aak74751 Human imm
ID	ADH13942	ADN12120	ADO03802	AD003803	ABL33652	ABL33653	ACN44486	ABK52382	AAS34422	ADN41808	ABX08336 07	ADJ25985 07	ADN97989_07	ADO50281_07	AAS70462	AAS72056	ACA30296	ACN44070	AAS61419	AAK74751
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Score	300	296.8	296.8	296.8	204	194.4	36.8	35.4	35	35	34.4	34.4	34.4	34.4	33.8	33.8	33.6	33.2	32.8	32.8
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Aak68958 Human imm Adk72196 Antimicro Adk72243 Antimicro Aal04311 Human rep Aag8248 P-selecti Aaa34226 Human ade Adf21048 Human low Ab296742 Human low Ab296591 Human low Ab296591 Human nuc Abd20591 Human pul Aas3411 DNA encod Abg77404 Human SEL Acn4286 Human Gen Adg97337 Human Gan Adg97347 Human imm Adk73471 Human imm Aak73471 Human imm Aak73471 Human imm Adk73473 Human imm Adk73471 Human imm Adk73473 Human imm Adk73473 Human imm Adk73473 Human imm Adk7349 Axabidops Adh3265 Human gen Acn45154 Human gen Acn45159 Human gen Acn45159 Ovarian col	Ab117530 Drosophil Aas12439 DNA encod
	ABL17530 AAS12439
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36485 661 661 3196 4866 4866 4866 4866 18595 78025 105219 110469 262090 393 10159 84073 1496112 1496112 1496112	4199
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10000000000000000000000000000000000000	44 5

## ALIGNMENTS

ADH13942 standard; DNA; 300 BP

ADH13942

ADH13942;

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:5. Poustka A; Delius H, Disclosure; SEQ ID NO 5; 30pp; English. Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) ٦, ̈́ Roesl F, Soto U, Coy Zur Hausen H, Patzelt WPI; 2002-165895/22. cervical carcinoma Homo sapiens. EP1170372-A1. 09-JAN-2002. 

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RESULT 3
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                                                                                                ö
                                                                                                                                                                                                                                                240
                                                                                                                                                             TTAACATGCCTCAAGTACTCCTATCATTTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
                                                                                                                                                                              TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
EBV-associated cancer; Hodgkin's lymphoma, nasopharyngeal carcinoma;
gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma;
parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated
                                                                                                                                         9
      the treatment
                                                                                                                                                                                                                                                           TCTAAGGTCTTTGGGTTTTTATCAGTGTGCCTTCTGTAGTTTTCTGAGGAAATCTAAGGCAC
                                                                                                                                                                                                                         rchaaggichtigggrittharcagigcettcigiagirtcigaggaaarchaaggcac
                                                                                                                                                                                                                                               AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG
                                                                                                                                                                                                                                                                                        TCCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT
                                                                                                                                  pharmaceutical composition of the invention is useful for the treat of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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                                                                               Length 300;
                                                                                                  0; Indels
                                                         Sequence 300 BP; 92 A; 62 C; 67 G; 79 T; 0 U; 0 Other;
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                                                                               , DB 6;
4.6e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                               100.0%; Score 300; D
100.0%; Pred. No. 4.6
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    ADN12120 standard; DNA; 3221 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    MCP1 gene promoter region
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-295406/27.
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004027036-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ambinder RF,
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ADN12120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy; promoter.
gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma, pastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma, parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present sequence represents a nucleotide sequence associated with the cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Cc12 promoter region used for gene knockout animal models SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testing candidate drug for treating age-related macular degeneration, administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, a malyzing development or regression of drusen and/or lipofuscin accumulation in eye.
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                   Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         Score 296.8; DB 12; Pred, No. 1.3e-84; Dred, No. 1.3e-84; Dred 2; Indels
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                                                                                                                                                                                                                                                                          98.9%;
llarity 99.3%;
Conservative (
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 298; Conserv
                                                                                                                                                                                        of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                 1445 AAGGAGGAGGCAGTGGGCTAGGAGAATGGAGAATCTAGAATTTTAAACTCAGCCCAGCCA 1504
             This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, CCr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Cc12 promoter region DNA of the invention.
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                                                                                                                                                                                                                                                                                        DB 12; Length 3221;
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                                                                                                                                                                                                                                                    Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                      Score 296.8; DB 12; Length
Pred. No. 1.3e-84;
0; Mismatches 2; Indels
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99.3%;
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Best Local Similarity
Matches 298; Conserv
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Testing candidate drug for treating age-related macular degeneration, by

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6488
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Cc12-deficient, Ccr2-deficient knockout mouse, and or regression of drusen and/or lipofuscin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6369 FCFAAGGFCTTTGGGFTTTTATCAGTGGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 296.8; DB 12; Length
Pred. No. 2.1e-84;
0; Mismatches 2; Indels
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                                                                          4; 64pp; English
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Best Local Similarity 99.3%;
Matches 298; Conservative
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administering drug to
analyzing development
accumulation in eye.
                                                                            Disclosure; SEQ ID NO
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Olek A,

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                                                                                                                                                                                                                                                                                                                                                                                            of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurotibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                  fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5926 BP; 1554 A; 55 C; 1492 G; 2825 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
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); Mismatches 66;
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78.0%;
                                                                                         30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                   02-JUL-2001; 2001WO-EP007537
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                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                         (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                         methylation.
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Matches 234;
                   03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3813 irraaggirririsggriririatragrigiririrgiagriririsaggaaairiaaggrar 3872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3933 ITTTTTGGAAATTAAGAAGGAAGTTAGGAGAATAGTTGTTATAATTAGGGATGAATTTTT 3992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, necoascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumacoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTAAGGTCTTTGGGTTTTTAATCAGTGTGCTTCTGTAGTTTTCTGAGGAAATCTAAGGCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation, antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidiabetic; antipsoriatic; antiantinflammatory; cancer; eye disease; arteriosclerosis; anaemia; autinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                               chemically modified gene, useful for associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCTTGGAAATTAAGAAGGCAAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAGGAGGTAGTGAGGAGATCGAGAGTTAGAATTTTAAATTTAGTTTAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGAGGAGGAGTGGGCTAGGAGAATCGAGAGTCAGAATTTTAAACTCAGCCCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 204; DB 6;
80.0%; Pred. No. 1.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                     Nucleic acid comprising fragment of diagnosis and treatment of diseases methylation.
                                                                                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL33653 standard; DNA; 5926
        30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.0
Best Local Similarity 80.0
Matches 240; Conservative
                                                                                                          Piepenbrock C,
                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                 WPI; 2002-130909/17
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Length 5926;

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Morris DW;

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1079 AACTCCAAGSTTTGTGCCTTCCTTCCAGCCGTCTCTGTCGCGATTTTAGGAAACCATCA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AATTCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1019 CCGAAATTGGGAATTTCGAAGTGCCTTACCATTCCACATATACTCCTGTATCGTGTTATC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a fucose-specific lectin protein with enzymic activity useful for foodstuffs, drugs and cosmetics. This sequence encodes a fucose-specific lectin protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 CACAACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, foetal tissue antigen, ds, antiinflammatory, neuroprotective,
immunomodulator; cardiovascular; cytostatic, nephrothropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fucose-specific lectin protein with enzymic activity useful for foodstuffs, drugs and in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 2122 BP; 575 A; 484 C; 505 G; 558 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA for a novel foetal antigen, SEQ ID No 1846.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 3-4; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS34422 standard; DNA; 32186 BP.
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Best Local Similarity 54.1%;
Matches 72; Conservative (
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993. .1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105675 TTCACAGTCAACACGCAATGAAAGTTTATGAATTTCTCTTTTTATGCTTTGAAGACATA 105616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 ITTAAACTCAGCCCAGCCATTAACATGCCTCAAGTACTCCTATCATATTGTAAGAGACA 101
                                                                                                                                                                                                                Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fucose-specific lectin protein; enzyme; foodstuff; drug; cosmetic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 204621 BP; 53683 A; 43334 C; 43489 G; 57468 T; 0 U; 6647 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105615 ATACTTATGGAGACCCAATTCAGAAGTCATGCGATTTTCAGCAGGGTGAGTC 105564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 ACAGITCACTGAAATGAATTCTAAGGICTTTGGGTTTTTATCAGTGTGCTTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .Match 12.3%; Score 36.8; DB 11; Length 204621; Local Similarity 58.0%; Pred. No. 2.9; es 65; Conservative 0; Mismatches 47; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463. .1613
/ttag= a
/product= "fucose lectin protein"
463. .498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding fucose-specific lectin protein.
                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 958; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK52382 standard; DNA; 2122 BP
              28-FEB-2003; 2003WO-US006235
                                                    01-MAR-2002; 2002US-00087192
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499. .549
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550. .726
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                                                                                          (SAGR-) SAGRES DISCOVERY
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14-SEP-2000; 2000US-0234265P.

21-SEP-2000; 2000US-023497P.

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217-NOV-2000
       cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; carder; cardiovascular disorder; cardiavascular disorder; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                    2000US-0179065P.
2000US-018656P.
2000US-0186550P.
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44-FEB-2000; 2

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28-JUN-2000; 2

28-JUN-2000; 2

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                                                                                                                Homo sapiens
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antiallergic; antiasthmatic; gastrointestinal; anticoagulant;
thrombolytic; antiatrerioscelerotic; cardiant; cytosfatic; nephrotropic;
cardiovascular; respiratory; gene therapy; secreted protein;
cardiovascular; respiratory; gene therapy; secreted protein;
cardiovascular; respiratory; gene therapy; secreted protein;
cardiovascular; respiratory; gene therapy; secreted protein;
cardiovascular; semminodeficiency; Chedlak-Higashi syndrome;
cardiomanne disease; systemic lupus erythematosus; rheumatoid arthritis;
cardiovascular; asthma; inflammatory; condition;
cardiovascular; sessionshila; thrombosis; thromboembolism;
alherosclerosis; myocardial infarction; angina; anaemia;
chronic kidney failure; renal tubular acidosis; kidney stone;
cardiovascular disorder; respiratory disorder; human; ds.
antiarthritic; antirheumatic; neuroprotective; antianaemic; muscular; antiallergic; antiasthmatic; gastrointestinal; anticoagulant;
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970S-0051919P-
970S-0051920P-
970S-0051926P-
970S-0051928P-
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97US-0058664P.
97US-0058785P.
98WO-US013684.
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SOPPET D R.
RUBEN S M.
KYAW H.
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ZENG Z.
LAFLEUR D V
MOORE P A.
SHI Y.
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EBNER R.
BIRSE C E
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(BIRS/)
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    The invention relates to novel mucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliotate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic for in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune to diseases e.g. rheumatorid arthritis, hyperproliferative disorders e.g. cardiovascular disorders e.g. cerebral ischeemia, angiogenesis, carrest, cerebrovascular disorders e.g. cerebral ischeemia, angiogenesis, necylasms of the breast or liver, cardiovascular disorders e.g. cerebral ischeemia, angiogenesis, or arrest, cerebrovascular disorders e.g. cerebral ischeemia, angiogenesis, cerevous system disorders e.g. Alzheimer's disease, infections caused by charteria, viruses and fungi and ocular disorders e.g. corneal infection.

The polypoptides can also be used to aid wound healing and epithelial colleration, to prevent skin aging due to subburn, to maintain or organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease corrects and other nutritional components. Numerous also be used as a food additive or preservative to increase or decrease corrects and disorders and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and component but a gene encoding a foetal antigen of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7072 CTCTAATATACATTTAAAATTTTTCACAATAAAAATTTAAAAATTTTGCCTTGGATCTTT 7013
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                                                                                                                                                                                                                                     New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and respiratory systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 CTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAATTCTAAGGTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCACAACTGAGGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulator; immunosuppressive; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1846; 642pp; English.
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                                                                                                                                                           Ruben SM;
              08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
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53.2%;
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2000US-0251869P
                                                                           05-JAN-2001; 2001US-0259678P
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nes 74; Conservative
                                                                                                                                                           Barash SC,
                                                                                                                                                                                               WPI; 2001-488782/53.
                08-DEC-2000;
08-DEC-2000;
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of ADN97989 from base 700001 (Human phosphodiesterase 4D genomin 17 fragments LOCUS ADN97989 Accession Adn97989
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Pred. No. 13;
0; Mismatches 61;
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Pred. No. 13;
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                                                                                                         Conservative
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ADN97989 07
Continuation (8 of 17) of
Continuation split into 17
WP ACHORIC SPECTOR Name
WP ADN97989 00
WP ADN97989 02
WP ADN97989 03
WP ADN97989 04
WP ADN97989 04
WP ADN97989 04
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ABX08336_14
ABX08336_15
ABX08336_16
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Matches
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                                                                                                                                                                                                     The invention describes novel human secreted proteins and the nucleotides concoling them. The polynucleotides are useful in chromosome identification, for radiation hybrid mapping, in controlling gene identification, for radiation hybrid mapping, in controlling gene cypression, in gene therapy or as molecular weight markers. The expression, in gene therapy or as molecular weight markers. The columnication of the immune system, immunodeficiencies, e.g. preventing diseases of the immune system, immunodeficiencies, e.g. preventing syndrome, autolimune diseases, e.g. systemic lupus corpressions, rheumatoid arthritis, multiple sclerosis, haemolytic crythematous, rheumatoid arthritis, multiple sclerosis, haemolytic corprised as a stimulator of B call responsivenes to pathogens or as an columniant for treating or preventing blood-related disorders, e.g. activator of T calls. The polynucleotides and polypeptides are also coinophila, thrombosis, thromboembolism, atherosclerosis, myocardial cosinophila, thrombosis, thrombosmbolism, atherosclerosis, myocardial cosinophila, thrombosis, thrombosmbolism, atherosclerosis, myocardial concers), renal disorders (chronic kidney failure, renal tubular collisorders (thronic kidney failure, renal tubular collisorders (thronic failorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory collisorders. The sequence represents a novel human secreted protein disorder form the US patent of fice at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13681 AAİTTTİTİACAİCACİQCCCAİAİAİİİİİİİİİ ABAAAAAİACIĞIAAAİTİĞAATA 13622
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                                                                                                     New isolated nucleic acid encoding human proteins, useful for treating, preventing or diagnosing e.g. rheumatoid arthritis, multiple sclerosis, anemia, inflammatory bowel disease, atherosclerosis, cancers, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                 Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 38855 BP; 11951 A; 6822 C; 6960 G; 13122 T; 0 U; 0 Other;
                                   Zeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 38855;
                                 Soppet DR, Ruben SM, Kyaw H, Li Y,
Shi Y, Olsen H, Ebner R, Birse CE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                       Disclosure; SEQ ID NO 930; 372pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35;
Pred. No. 5
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1 Similarity 53.2%;
74; Conservative (
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Sequence split into 17
                                            Rosen CA,
Moore PA,
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Best Local Similarity
                                                                                     WPI; 2004-225733/21.
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ABX08336_07
Continuation (8 o
                                              Fischer CL,
Lafleur DW,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed crivity of (II) is useful in gene therapy techniques to restore normal activity of (II) so to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics. Forensics disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences has and products dependent on DNA and and a contact the sequences has a product dependent on DNA and a contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact contact c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                          DNA encoding novel human diagnostic protein #6266.
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23-AUG-2000; 2000US-00649167
                                       13-FEB-2002 (first entry)
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P-PSDB; ABG06275.
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les 65; Conserv
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                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                       Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	CR231209 Reverse s	AZ446937 1M0243N04	CL051289 CH216-73K	CE726528 tigr-gss-	CC314654 TAM32-17J	AI857124 MBNAAd-23	CL092596 ISB1-22D2	CG226877 OG0CZ03TH	CG360051 OG0EZ60TH	CG222409 OG0FU36TH	CC408141 PUHIF57TD	CC408138 PUHIF57TB	CL991997 ZMMBH£000	CL987077 ZMMBHe000	CL985353 ZMMBHe000	CL368806 RPCI44 28	AQ795241 nbxb0055N	B72588 RPCI11-9J17	CE290785 tigr-gss-	AG175765 Pan trogl	_	BF604634 270544 MA	BB620693 BB620693	CR041049 Reverse s
SUMMARIES	ID	CR231209	A2446937	CL051289	CE726528	CC314654	AI857124	CL092596	CG226877	CG360051	CG222409	CC408141	CC408138	CL991997	CL987077	CL985353	CL368806	AQ795241	B72588	CE290785	AG175765	AZ757570	BF604634	BB620693	CR041049
	Query Match Length DB	737 9	648 8	1115 9	721 9	1043 8	675 1	1114 9	731 9	819 9	849 9	884 8	935 8	985 9	1027 9	1058 9	728 9	723 8	478 8	631 9	682 9	293 8	468 2	686 2	6 699
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	Score	43.4	39	37.8	37.4	37.2	37	37	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.2	36	35.8	35.8	35.8	35.6	35.6	35.6	35.4
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E (remitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
A physical map of the xenopus tropicalis genome
Onpublished (2003)

Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000
Seq primer: Sp6 ATTTAGGTGACTATAGG
Class: BAC ends
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tigr-gss-dog-17000329818790 Dog Library Canis familiaris genomic, genomic survey sequence.
CE726528
GE726528.1 GI:37066648
                                                                                                                                                                                                                                   CL051289 1115 bp DNA linear GSS 31-DEC-2003 CH216-73X13 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-73X13, genomic survey sequence.
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/cell line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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12.6%; Score 37.8; DB 9; Length 1115;
Best Local Similarity 54.7%; Pred. No. 5.4;
Matches 75; Conservative 0; Mismatches 62; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-73K13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 67
High quality sequence stop: 334.
Location/Qualifiers
                           268 GAGCATAGCTGCCATAACCAGGG 290
                                                                               193 AAGTATGTCTGTTATAAACAAGG 171
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AUTHORS
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Bukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1. (Dases 1 to 648)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacree,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Longachian scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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University of Utah

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Imboratory Mouse DNA Resource (http://www.jax.org/resources/dccuments/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase and T4 polymerase (plant) T6 polymerase and T6 polymerase and T6 polymerase and T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T7 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6 polymerase (plant) T6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
AZ446937 648 bp DNA linear GSS 04-OCT-2000 IM0243N04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0243N04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42Lv; Purified genomic DNA from M.musculus CS7BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 TGCTTCTGTAGTTTCTGAGGAAATCTAAGGCACAACTGAGGAATGAAGTCAGGCTTTCCA
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13.0%; Score 39; DB 8; Length 648;
Best Local Similarity 54.5%; Pred. No. 2.1;
Matches 78; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: N column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="genomic DNA"
/train="C57BL/"
/db xref="taxon:10090"
/clone="UUGC1M0243N04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 648.
Location/Qualifiers
                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                          AZ446937.1 GI:10598239
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AI857124

MBNAAA-239SAC Necator americanus (parasitic nematode) mixed adult
Necator americanus cDNA clone MBNAAG-239 5' similar to from Necator
americanus EST cluster NAC00239, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida, Ancylostomatoidea, Ancylostomatidae, Bunostominae, Necator.

1 (bases 1 to 675)

Boub, J., Loukas, A., Pritchard, D. and Blaxter, M.

A survey of genes expressed in adults of the hookworm Necator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/clone_lib="Necator americanus (parasitic nematode) mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Zap Express; Site_1: BcoRI (5'end);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +44 131 650 6760

Fax: +44 131 670 5450

Fax: +44 131 670 5450

Email: mark.blaster@ed.ac.uk

The Nocator americanus EST dataset (including the NAC clustering information) is available on the www at http://www.ed.ac.uk/

mbx/NocatorEST.html

PCR PRIMERS

FORWARD: M13 Reverse (AGCGGATAACTATTCACACAGGA)

BACKWARD: M13 FORWARD (GGCCAGGSTTTCCCAGTCACGCC)

Seg primer: SAC (GGGAACAAAGCTGGAG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AGCCATTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAA
                                                                                                                                                                          Length 1043;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AGTCCTGCATGGACTTGGGTTTACTATCAAGGTATTTC 74
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                                                                                      /mol_type="genomic_DNA"
/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="TAM32-17J9"
                                                                                                                                                                                                                                                                                                                                                            Score 37.2;
Pred. No. 8;
                                                               organism="Gallus gallus"
  ity sequence stop: 535.
Location/Qualifiers
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/db xref="taxon:51031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Blaxter ML
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    High quality
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TAM32-17J9_Sp6.1 TAM32 Gallus gallus genomic clone TAM32-17J9,
genomic survey sequence.
                                                                                                                                                                                                                                                            The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 721)
Kirkness, E. R., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
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Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Wallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="Standard Poodle"
/strain="Standard Poodle"
/bx xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                              Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Canis familiaris"
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Gallus gallus
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Canis familiaris
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Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Xenopodinae; Metrachia; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Xenopus tropicalis genome

I (bases 1 to 1114)

Xenopodinae; Xenopus tropicalis genome

I (phyblished (2003)

Contact: Richard K Wilson)

Contact: Richard K Wilson of Medicine

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 75000 Std Error: 0.00

Seg primer: TAATACGACTCACTATAGGG
Site_2: XhoI (3'end); Necator americanus is a human hookworm, responsible for debilitating anaemia. The library was constructed from mRNA from N.americanus adults (Nottingham strain) maintained in hamsters."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                 CL092596 1114 bp DNA linear GSS 05-JAN-2004 ISB1-22D23_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-22D23,
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/db xrefpe="genomic blv4"
/clone="ISB1-22D23"
/clone=lib="ISB1"
/note="Yector: pBeloBAC11; ISB-1 Xenopus tropicalis
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                               Length 1114;
                                                                                                     12.3%; Score 37; DB 1; Length 675;
.larity 58.7%; Pred. No. 8.2;
Conservative 0; Mismatches 45; Indels
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    1114
/organism="Xenopus tropicalis"

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Pred. No. 9.3;
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High quality sequence start: 5
High quality sequence stop: 323.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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CL092596.1 GI:40586231
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Best Local Similarity 53.03
Matches 79; Conservative
                                                                                                                             Local Similarity
les 64; Conserv
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                                                                                                            Query Match
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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Matches
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CG360051 819 bp DNA linear GSS 26-AUG-2003
OG0EZ60TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0703124,
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COSCZ03TH ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0690A06, genomic survey sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 819)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 icttrairaaitcacicaattgatctaiitccciatggcacaittiririaaatigiaia 306
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                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 731)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGGCZ03TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 TCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCTCAAGTACTCCTATCATATTTGTA
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/clone="Velcory" 0.7 1.5 KB"
methylation filtered genomic DNA library"
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Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
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50.6%; Pred. No. 13;
tive 0; Mismatches
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survēy sēguence.
CG360051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Whitelaw
                                                                                                                                          CG226877.1 GI:34126765
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Class: sheared ends
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Fax: 301-838-0208
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Gaps

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Length 849;

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B84 bp DNA linear GSS 19-MAY-2003 PUHHF57TD ZM 0.6_1.0 KB Zea mays genomic clone ZMWBTa457118, genomic survey sequence.
                                                                                                                                                                                                                                                                                                            197 TCTTTATAATTCACTCAATTGATCTATTTCCCTATGGCACATTTTTTTAAATTGTATA 256
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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COT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 GIGGITICATAATAATIGIATIGAAAAAAACAAIGCIGAAGCAAGAGITITAAA 370
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Atrain="B17"
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/clone="ZMMBMa0708F23"
/clone="ZMOT"
/note="Voctor: PBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 884)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                           86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.4; DB 8; Length 8 Pred. No. 13; 0; Mismatches 86; Indels
                                                                                                                                                                                       DB 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD
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; Pred. No. 13;
0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC408141.1 GI:30888231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_GSSs: PUHIF57TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%;
50.6%;
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Local Similarity 50.6%;
es 88; Conservative
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Best Local Similarity
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Zea mays
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JOURNAL
COMMENT
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CC408141
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OG0FU36TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0708F23,
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1 (bases 1 to 049)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGOFU36TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 AGAGACAACAGCTTCACTGAAATGAATTCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381
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Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGGEZ60TV

Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AGACTGAAATTTTCTGTTAATGGTAACATAATTTGTTGTTCTTTTTGTATTTTGCTATA
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methylation filtered genomic_DNA library"
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                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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REFERENCE AUTHORS

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14, J., Sanhiguel, P., Liu, R., Haller, K., Soderlund, C. and Bennetzen, J.
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Department of Genetics, C426a Life Sciences Building, Athens, 130602, USA
Tel: 706-542-3698
Fax: 706-583-0972
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Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennetzen,J.
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/mol type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                     Email: maize@uga.edu
Plate: 0003 row: d column: 22
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Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
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Contact: Jeff Bennetzen
GI:52560075
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CoT selected genomic DNA library"
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Tel: 301-838-5843
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/mol type="genomic DNA"
/strain="B73"
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Fax: 301-838-0208
Emall: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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Other GSS8: PUHIF57TD
Contact: Cathy Whitelaw
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Ma.J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and Bennetzen, J.
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The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
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The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, 30602, USA
TEL: 706-542-3698
Fax: 706-583-0972
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Acganism="Zea mays"
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/cultivar="R73"
/db_xref="taxon:4577"
                                                                                  Email: maize@uga.edu
Plate: 0003 row: k column: 03
Class: BAC ends.
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Unpublished (2004)
Contact: Jeff Bennetzen
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Fax: 706-583-0972
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Matches 88; Conserv
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                             567 rcrrraraarrcacrcaarrgarcrarrcccrarggcacarrrrrrraaarrgrara
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                                                                                                                                                                            12.1%; Score 36.4; D 50.6%; Pred. No. 14; ive 0; Mismatches
/clone="ZMMBHe0001e22"
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Matches 88; Conserv
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Search completed: August 4, 2005, 14:32:29 Job time : 1423.95 secs This page Blank (Usbjo)

us-09-899-276c-5.rni

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM nucleic - nucleic search, using sw model Run on:

August 4, 2005, 07:01:49; Search time 61.8219 Seconds (without alignments) 7940.282 Million cell updates/sec US-09-899-276C-5 300

l aaggaggaggcagtgggcta......ataaccagggatgaacttct 300 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Perfect score: Sequence: Scoring table:

1202784 segs, 818138359 residues Searched:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			*			SOFTWANTES		
	ult No.	Score	Query Match	Le	DB	ID	Description	
; o	-	35.6	11.9	15331	4	US-09-949-016-13355	Sequence 13355, A	
υ	~		11.4	601	4	-949-016-1	_	
υ	ო	34.2	11.4	601	4	US-09-949-016-152884		
U	4	٠	11.4	601	4	US-09-949-016-152885		
υ	S	34.2	11.4	166698	4	US-09-949-016-16038	Sequence 16038, A	
	9	33.8	11.3	152524	4	US-09-949-016-12683	Sequence 12683, A	
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	æ	33.4	11.1	17763	4	US-09-949-016-12637		
	σ	33.4	11.1	17764	4	US-09-949-016-13143	13143,	
υ	10	32.6	10.9	4866	-	US-08-110-158-5		
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	13	32.4	10.8	133613	4	US-09-949-016-15824	Sequence 15824, A	
υ	20	32.2	10.7	601	4	US-09-949-016-85649	8564	
U	21	32.2	10.7	5483	4	US-09-853-450-47	Sequence 47, Appl	
U	22	32.2	10.7	340380	4	US-09-949-016-14179	141	
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	56	32	10.7	69764	4	US-09-949-016-15638		
	27	32	10.7	212449	4	US-09-949-016-15419	Sequence 15419, A	

; Sequence 152883, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION: , APPLICANT: VENTER, J. Craig et al. ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

RESULT 2 US-09-949-016-152883/c

Sequence 12705, A Sequence 17550, A	Sequence 130167,	Sequence 80, Appl	Sequence 16813, A	Sequence 17175, A	Seguence 1957, Ap	Sequence 508, App	Sequence 30, Appl	Sequence 13799, A	Sequence 17, Appl	Sequence 15920, A	Sequence 12553, A	Sequence 13210, A	Sequence 14588, A	Sequence 14589, A	Sequence 17119, A	Seguence 16297, A
US-09-949-016-12705 US-09-949-016-17550	US-09-949-016-130167	US-09-220-132-80	US-09-949-016-16813	US-09-949-016-17175	US-09-583-110-1957	US-09-107-433-508	US-08-569-166-30	US-09-270-767-13799	US-08-961-527-17	US-09-949-016-15920	US-09-949-016-12553	US-09-949-016-13210	US-09-949-016-14588	US-09-949-016-14589	US-09-949-016-17119	US-09-949-016-16297
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10.7	10.5	10.5	10.5	10.5	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4
33	31.6	31.6	31.6	31.6	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2
28 29	30	c 31	c 35	33	c 34	c 35	c 36	c 37	38	39	40	41	c 42	c 43	c 44	45

## ALIGNMENTS

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Sequence 13355, Application US/09949016

Sequence 13355, Application US/09949016

Sequence 13355, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 1355

SEQ ID NO 1355
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Pred. No. 0.28;
0; Mismatches 74; Indels 0;
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Best Local Similarity 51.9%;
Matches 80; Conservative C
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; ORGANISM: Human
US-09-949-016-13355
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US=09-949-016-16038/C
; Sequence 16038, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHEMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR PALLICATION NUMBER: 60/241,755
; PRIOR PALLING DATE: 2000-10-03
; PRIOR PAPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTWARE: RESELECT FOR Windows Version 4.0
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,758

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARD OF SEQ ID NOS: 207012

SEQ ID NO 152885

LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34.2; DB 4;
Pred. No. 0.16;
0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 TGAGGAAATCTAAGGCACAACTGAGGAATGAAGTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.2; DB Pred. No. 3.1; 0; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16038
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60.0%;
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Best Local Similarity 60.03
Matches 57; Conservative
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-152885
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ORGANISM: Human
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELLORICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELLORICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-0-09-08
PRIOR PELLOR OF APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Pred. No. 0.16;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34.2; DB 4; Length 601; Pred. No. 0.16; 0; Mismatches 38; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 TGAGGAAATCTAAGGCACAAATGAAGTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 CCAAGAATTCTAAGGAACATAGCTTCAATGAAATC 456
             FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 152883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-949-016-152885/c
US-09-940-016-152885/s
; Sequence 152885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 152884, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 60.0%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0%
Matches 57; Conservative
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US-09-949-016-152883
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LENGTH: 601
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Indels

38;

Length 601;

Gaps

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38; Indels

Length 166698;

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Sequence 12637, Application US/09949016

Batent No. 681233

GENBRAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRAESE PRIOR WINDOWS Version 4.0

SEQ ID NO 12637

LENGTH: 17763
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Sequence 13143, Application US/09949016
Sequence 13143, Application US/09949016
Sequence 13143, Application US/09949016
SERVERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11704 rcrigirgaarigarcccriraccaraargragiggccrirgicrcrirrigarcriffgrg 11763
                                               72 CAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAATTCTAAGGTCTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 TGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATGTCCCTTGGAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 TTGGGTTTTTATCAGTGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCACAACTGAGGAA
12 AGTGGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 TCAAGTACTCCTATCATATTTGTAAGACAACAGTTCACTGAAATGAATTTCTAAGGTCT
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                                                                                                                                                                                                132 TGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33.4; DE
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.18;
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Best Local Similarity 48.78
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US-09-949-016-12637
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US-09-949-016-13143
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                                                                                 Sequence 12683, Application US/09949016

Sequence 12683, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

FRICATE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12683

LEGGTH: 155224
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: us/09/949, ule

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AGTGGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.8; DB 4; Length 152524; Pred. No. 4.1; 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.8; DB 4; Length 152524;
Pred. No. 4.1;
0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2950 TGTGTCTCTATAAGGCAGAACGTGTTCTGTAAGAGTAAACCCAAG 2994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 TGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARRS: FastSEQ for Windows Version 4.0
SEQ ID NO 13194
LENGTH: 152524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13194, Application US/09949016
Patent No. 6812339
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Best Local Similarity 50.3%;
Matches 83; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.3%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
, ORGANISM: Human
US-09-949-016-12683
                                                                  -09-949-016-12683
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US-09-949-016-13194
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ORGANISM: 1
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Gaps

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DNA (genomic)
                                                                             Best_Local Similarity
Matches 59; Conserv
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  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Human
US-09-949-016-16142
            US-08-110-158-5
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                                                              Query Match
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                                                                                                                                                                                                                                                                                                              71 TCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAATTCTAAGGTCT 130
                                                                                                                                                                                                                                                                                                                                                                                                131 TIGGGITITITATCAGIGIGCITCTGIAGITITCTGAGGAAATCIAAGGCACAACTGAGGAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 TGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATGTCCCTTGGAA 250
                                                                                                                                                                                                                              11.1%; Score 33.4; DB 4; Length 17764; 48.7%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gequence 5, Application US/08110158
; Patent No. 560821
; GENERAL INFORMATION:
    APPLICANT: McEver, Rodger P.
    APPLICANT: McEver, Junitang
    TITLE OF INVENTION: Expression Control Sequences of the
    TITLE OF INVENTION: P-Selectin Gene
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Patrea L. Pabst
    STREET: 1100 Peachtree Street, Suite 2800
    CITY: Atlanta
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/110,158

FILING DATE: 19930820

CLASSIFICATION NUMBER: US 07/320,408

FILING DATE: OB-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Pablet, Patrea L.

REGISTRATION NUMBER: 31,284

TELECOMMUTCATION INFORMATION:

TELEPHONE: (404)-815-6508

TELEPHONE: (404)-815-6555

INFORMATION FOR SEQ ID NO: 5:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                       0; Mismatches
    PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13143
LENGTH: 17764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4866 base pairs
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.73
Matches 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11764 GTTTAAA 11770
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                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                           US-09-949-016-13143
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US-08-110-158-5/c
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Sequence 16442, Application US/09949016

Fatent No. 6812339

Fatent No. 6812349

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPIOR PRIOR POLICATION NUMBER: 60/231,498

NUMBER OF SEC ID NOS: 207012

SOFTWARE: FRASESE FRASESEQ for Windows Version 4.0

SEQ ID NO 16142

LENGTH: 45323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                 3105 CTATCAGCATCATGAGAACAGAATAATACACTCAGCAATGTGAATAATAAGGATAATAAT 3046
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                                                                                                                         18 CTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCTCAAGTA
                                                                 Gaps
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Pred. No. 5.5;
      Length 4866;
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                                                                    44;
Score 32.6; DB 1;
Pred. No. 1.7;
0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.3%;
Matches 59; Conservative C
   ch 10.9%;
il Similarity 57.3%;
59; Conservative
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Search completed: August 4, 2005, 14:40:55 Job time: 67.8219 secs
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US-09-949-016-17009
                                                                                                                                                                                                                        TYPE: DNA
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Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 00/09/949,016

CURRENT PAPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTENCE OF WINDOWN VETSION 4.0
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: u2(09)949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                  30938 TTAAAGTCTCCCATTATTATTGTGGGAGTCTAATTCTCTTTGTAGGTCTCTAAGGACT 30879
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Pred. No. 8.1;
0; Mismatches 44; Indels 0;
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Pred. No. 7.3;
0; Mismatches 44;
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Patent No. 6812339
                                                                                                                                                            ) OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15896
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Best Local Similarity 57.3%;
Matches 59; Conservative
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Best Local Similarity 57.3%;
Matches 59; Conservative
                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(76472)
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                                               TYPE: DNA
ORGANISM: Human
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US-09-949-016-17484
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SEQ ID NO 15896
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LENGTH: 92155
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                                                                                              FEATURE:
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RESULT 15
US-09-949-016-17009

i Sequence 17009, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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10.9%; Score 32.6; DB
Best Local Similarity 55.9%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches
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Pred. No. 8.1;
0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASELSEQ for Windows Version 4.0
SSOFTWARE: PASELSEQ for Windows Version 4.0
LENGTH: 92276
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17009
LENGTH: 205163
                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(92276)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12166
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Best Local Similarity 57.3%;
Matches 59; Conservative
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August 4, 2005, 08:04:16; Search time 535.142 Seconds (without alignments) 3633.986 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

APPLICANT: COV, Johannes
APPLICANT: Finzer, Patrick
APPLICANT: Delius, Hajo
APPLICANT: Delius, Hajo
APPLICANT: Delius, Haio
APPLICANT: Delius, Harald
APPLICANT: Zur Hausen, Harald
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APPLICANT: Zur Hausen, Harald
CURRENT PILING DATE: Zur Harald
NUMBER OF SEQ ID NOS: 12
SSOFTWARE: FastSEQ for Windows Version 4.0

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Length 300;

Query Match 100.0%; Score 300; DB 9; Length 3 Best Local Similarity 100.0%; Pred. No. 5e-88; Matches 300; Conservative 0; Mismatches 0; Indels

TYPE: DNA ORGANISM: Homo sapiens

US-09-899-276-5

SEQ ID NO 5 LENGTH: 300

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SUMMARIES	ID	9 US-09-899-276-5	US-10-027-632-121412	US-10-027-632-121412	US-10-685-705-3	US-10-685-705-4	US-10-311-455-1625	US-10-311-455-1626
	98	6	13	11	19	19	15	15
	Query Match Length DB ID	300	934	934	3221	11793	5926	5926
dp	Query Match	100.0		99.9	98.9	98.9	68.0	64.8
	Score	300	299.6	299.6	296.8	296.8	204	194.4
	Result No.	-	7	m	4	S	9	c 7

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υ		'n.	H	2286	_	US-10-027-632-102218	equence 1022	
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		4	ä	69113	4.	US-10-067-514-1	e 1, Appl	
		4	ä	69113	-	US-10-419-723-1	1, Appl	
	19		11.5	1691140	22	US-10-868-397-1	Sequence 1, Appli	
		4.	ä		N	US-10-972-079-71139	equence 7113	
υ		4.	Η.	618	m	US-10-027-632-199837	1998	
υ		4	11.4	618		US-10-027-632-199838	1998	
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		m,	11.3	1924	_	US-10-027-632-104612	1046	
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O			ä		OI.	US-10-764-212-79		
		<u>.</u>	4	344548	m	US-10-087-192-334	334,	
	31		ä	009	C)	US-10-972-079-9597	9597	
		m	Η.	009	a	US-10-972-079-9598	9598	
		ς.	0	524	0	US-10-425-115-168400	1684	
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	35 3	2	10.9	2893	7	US-10-027-632-111626	1116	
-		2	ö	17918	7	US-10-221-613-382	382,	
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O		ς.	。	201	21	10-741-600-5543	5543	
		ď	。	3196	10	19-764-891-69	equence 6999	
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υ		Ċ,		53323	21	10-741-600-17	equence 1776	
O		3	10.9	78025	14	-020-141-9	equence 9, A	
		ď.		105219	13	10-087-192-658	equence 658,	
		32.4	10.8	009	22	S-10-972-079-95	equence 9599	
		'n	0	84073	13	-192-71	Sequence 712, App	
						ALIGNMENTS		
REST	SIII.T 1							
US-0	-09-899-2	3-94						
Se .	equence	5, Apr	plicat	ion US/	9899	3276		
- Pa	atent No.	, US20	002010	. USŽ0020106355A1				
5	GENERAL INFORMATION	INFORM	ATION:					
	APPLICANT:	-	Rosl, Fr	Frank				
	APPLICANT		oto, t	npaldo j				
	APPLICANT		οy, Jo	Coy, Johannes				
	APPLICANT		inzer,	Patrick	u			
	אייייייייייייייייייייייייייייייייייייי		erius,	Hajo Annom:	,			
	APPLICANT:		ouecae ir Hau	rouscha, Ammemaile zur Hausen, Harald	ple.			

265 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 324

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APPLICANT: University of Kentucky Research Foundation APPLICANT: UNIVERSIBA, Ambati TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
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                     DB 17; Length 934;
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Pred. No. 1.2e-87;
1; Mismatches 0;
                                                                                         US-10-027-632-121412; Sequence 121412, Application US/10027632; Publication No. US20030204075A9
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; Sequence 3, Application US/10685705
; Publication No. US20040177387A1
; GENERAL INFORMATION:
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Best Local Similarity 99.7'
Matches 299; Conservative
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                                                    61 TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
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Sequence 121412, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/189,676

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-108-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 121412

LENGTH: 934
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Pred. No. 1.2e-87;
1; Mismatches 0; Indels
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Best Local Similarity 99.7%;
Matches 299; Conservative
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| SENEMAL INFORMATION:
| APPLICANT: OLEK, Alexander
| APPLICANT: PIEPENBROCK, Christian
| APPLICANT: PIEPENBROCK, Christian
| APPLICANT: PIEPENBROCK, Christian
| APPLICANT: BELLIN, Kutt
| TITLE OF INVENTION: Cytosine methylation
| TITLE OF INVENTION: Cytosine methylation
| FILE REFERENCE: 5013-1014
| CURRENT APPLICATION NUMBER: US/10/311,455
| CURRENT FILING DATE: 2002-12-16
| PRIOR FILING DATE: 2001-07-02
| PRIOR FILING DATE: 2000-06-30
| PRIOR APPLICATION NUMBER: DE 10032529.7
| PRIOR APPLICATION NUMBER: DE 10043826.1
| RIOR APPLICATION NUMBER: DE 10043826.1
| RIOR APPLICATION NUMBER: DE 10043826.1
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                                    6369 TCTAAGGTCTTTGGGTTTTTTATCAGTGGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1625
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Best Local Similarity 80.0%; Pred. No. 8e-56;
Matches 240; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1625, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-311-455-1626/c
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US-10-311-455-1625
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Sequence 4, Application US/10685705

Sequence 10 No. US20040177387A1

Sequence 11 No. US20040177387A1

GENERAL INFORMATION:

APPLICANT: University of Kentucky Research Foundation

APPLICANT: University of Kentucky Research Foundation

APPLICANT: University of Kentucky Research Foundation

APPLICANT: University of Kentucky Research Foundation

TITLE OF INVENTION: Degeneration

FILE REFERENCE: 050229-0415

CURRENT APPLICATION NUMBER: US/10/685,705

CURRENT FILING DATE: 2003-10-16

PRIOR PLING DATE: 2003-10-16

PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.2

SEQ ID NOS: 10

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                                                                                                                                                                                                                                                                                                                                     98.9%; Score 296.8; DB 19; Length 3221; 99.3%; Pred. No. 1.7e-86;
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98.9%; Score 296.8; DB 19;
Best Local Similarity 99.3%; Pred. No. 3.2e-86;
Matches 298; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
FILE OF INVENTION: Degeneration
FILE REPERBRY;
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR PILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 321
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.3
Matches 298; Conservative
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-685-705-4
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GAAGTAGCCGCACAACCTACAATAATCATTTCACTTCTGTTGTTTCATTTGTAAAG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 ATCATTAAGGACACTTGGAGCAGAGGCTGAAAATGAAAGCAGAAATTCTGCTTCCCAGGA 293
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US-10-027-032-129-05.6

Sequence 129675, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Tellogation and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US 60/198,006

PRIOR FILING DATE: 2002-04-30

PRIOR PELING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR FILING DATE: 1999-00-28

PRIOR PILING DATE: 1999-00-28

PRIOR FILING DATE: 1999-00-28

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PRIOR FILING DATE: 1999-00-28

PRIOR FILING DATE: 1999-00-28

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PRIOR FILING DATE: 1999-00-28

PRIOR FILING DATE: 1999-00-38

PRIOR FILING DATE: 1999-00-38

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PRIOR FILING DATE: 1999-00-38

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PRIOR FILING DATE: 1999-00-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 ĠĠŖŔŢŔĊŢĠŖŔŢŔŖŔŢŢŖŔŢĠĊĠŢĊŢŢŢĊŖŖĊŖŢ-ŢĊŢŔŢĸĸŢĸŢĬŢĠŢĠ
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                                                                                                                                                                                                                                            Indels
                                                                                                                                                                               Score 40.4; DB 13;
Pred. No. 0.018;
0; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 TCCATAGCAAGGTATAYATTTC 214
                                                                                                                                                                                      13.5%;
52.3%;
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                                                                                                                                                                                          Query Match 13.59
Best Local Similarity 52.33
Matches 137; Conservative
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Best Local Similarity
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US-10-027-632-129675
                                                         TYPE: DNA
CRGANISM: Human
US-10-027-632-129675
SEQ ID NO 129675
                                 LENGTH: 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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      APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: D202-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1626
LENGTH: 5926
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GENERAL INFORMATION:

TITLE OF INVENTION: Polymorphisms in the Human Genome
FITTLE OF INVENTION: Polymorphisms in the Human Genome
FITTLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-4
PRIOR PILING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PELING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: Past-SEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5926;
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Pred. No. 1.1e-52;
0; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.8%;
Best Local Similarity 78.0%;
Matches 234; Conservative
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Best Local Similarity 58.0
Matches 65; Conservative
         ORGANISM: Homo sapiens
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US-10-027-632-89184
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                                                                                                                                                                           Query Match
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Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeQ for Windows Version 4.0
SEQ ID NO 6887
LENGTH: 290367
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recrerceace---raarreacrecritaagaaceagaraagaareragaaggereragi 236
                                                                                                                    352 arcariaaksakcastrissassaskaskaskaaaarisaaaariicussiricicassa 293
                                                                                                                                                                   158 GTTTCTGAGGAAATCTAAGGCACAACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mortis, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT PRILIG DATE: 2002-03-01
PRIOR PRILING DATE: 2002-03-01
PRIOR PLILNG DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR PLING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PARESEQ for Windows Version 4.0
LENGTH: 204621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
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12.3%; Score 36.8; DB
Best Local Similarity 58.0%; Pred. No. 4.4;
Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                               278 GCCATAACCAGGGATGAACTTC 299
                                                                                                                                                                                                                                                                                                    235 TCCATAGCAAGGTATAYATTTC 214
                                                                                                                                                                                                                                                                                                                                                                                                          US-10-087-192-958/c
; Sequence 958, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or
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NAME/KEY: misc feature
LOCATION: (1)....(290367)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1 US-10-719-993-6887)
                                                                                                                                                                                                                                                                                                                                                                       202461 TICACAGICAACACAGCAAIGAAAGTITAIGAATITCICITITITAIGCITIGAAGACATA 202402
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| Sequence 89184, Application US/10027632
| Publication No. US20020198371A1
| JERNERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: IO-Olymorphisms in the Human Genome FILE REPERENCE: 108827.129
| CURRENT APPLICATION NUMBER: US/10/027,632
| CURRENT APPLICATION NUMBER: US/10/027,632
| CURRENT APPLICATION NUMBER: US 60/218,006
| PRIOR APPLICATION NUMBER: US 60/218,006
| PRIOR PILING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/167,363
| PRIOR PILING DATE: 2000-03-29
| PRIOR PILING DATE: 12000-03-29
| PRIOR PILING DATE: 1909-09-28
| PRIOR PILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-08-09
| NUMBER OF SEQ ID NOS: 325720
| SCPTWARER FRAESEQ FOR WINGOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 ACAGITCACIGAAAIGAATICIAAGGICITIIGGGITITITAICAGIGIGCITC 153
                                                                                                                                                                                          12.3%; Score 36.8; DB 20; Length 290367; 58.0%; Pred. No. 5.2; cive 0; Mismatches 47; Indels 0; (
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Pred. No. 0.77;
1; Mismatches 34;
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Best Local Similarity 61.1%;
Matches 55; Conservative
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/0204.30

PRIOR APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR PELLING DATE: 2000-07-20

PRIOR PELLING DATE: 2000-03-20

PRIOR PELLING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR APPLICATION NUMBER: US 60/165,358

PRIOR PELLING DATE: 1999-11-28

PRIOR PILLING DATE: 1999-11-28

PRIOR PILLING DATE: 1999-104-08

PRIOR PILLING DATE: 1999-09-28

PRIOR PILLING DATE: 1999-08-09

PRIOR PILLING DATE: 1999-08-09

PRIOR PILLING DATE: 1999-08-09

PRIOR PILLING DATE: 1999-08-09

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         Polymorphisms in the Human Genome
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61.1%; Pred. No. 0.77;
iive 1; Mismatches 34;
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TITLE OF INVENTION: Polymorphisms in the Hum FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US/0/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR PILING DATE: 2000-07-12 PRIOR FILING DATE: 2000-07-12 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 2000-04-20 PRIOR PRIOR PELING DATE: 2000-04-20 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-24 PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-11-3 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-10-3 S0/146,002 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-28 PRIOR PRIOR PILING DATE: 1999-09-28 PRIOR PRIOR PILING DATE: 1999-09-28 PRIOR PRIOR PILING DATE: 1999-09-28 PRIOR PRIOR PILING DATE: 1999-09-28 PRIOR PRIOR PILING DATE: 1999-09-29 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
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Publication No. US20020198371A1
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Matches 55, Conservative
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ORGANISM: Human
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11.7%; Score 35.2; DB 13; Length 2286;

Query Match

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Squence 102218, Application US/10027632

Publication No. US2003020407589

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: DOLYMORER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-09-12

PRIOR FILING DATE: 2000-09-12

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-8

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SQCIWARE: FaetSEQ for Windows Version 4.0

SEQ ID NO 102218

FAURY TARRAMER: ARB
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                       Gaps
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11.7%; Score 35.2; DB 17; Length Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 115; Conservative 0; Mismatches 113; Indels
illarity 50.0%; Pred. No. 1.8;
Conservative 0; Mismatches 113; Indels
     Best Local Similarity
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Homo sapi
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - nucleic search, using sw model
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AC146488
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AC020914
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Maximum DB seq length: 200000000
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53.3 162139
53.1 142790
52.6 190149
52.6 210186
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Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
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1 (bases 1 to 147416)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiess chromosome 17, clone hRPK.215_E_13
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                                                                                                    Length 11793;
                                                                                                                                                   Indels
                                                                                                       ; Score 300; DB 9;
; Pred. No. 2.7e-76;
0; Mismatches 0;
8968. .>9073
/gene="MCP-1"
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC005549.1 GI:3598724
                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 300; Conservative 0
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/product="monocyte chemoattractant protein-1"
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zur Hausen,H. and Rosl,F.

zur Hausen,H. and Rosl,F.

poliferential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin on-tumorigenic HPV 18 positive cells: the role of the chromatin oncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                     PRI 18-OCT-2000
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Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Newenheimer Feld 506, 69120
                                                                                                                         300
         241 AATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA 300
                                                                                                                                                                                                                                                                                                Y18933.1 GI:10933860
MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                  oin(7610. .7685,8468. .8585,8968. .9073)
'gene="MCP-1"
                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                            IN 1793 bp DNA 1:
Homo sapiens MCP-1 gene and enhancer region.
Y18933
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Anilocation/Qualifiers
| Vigarianism=Homo sapiens|
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/gene="MCP-1"
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/gene="MCP-1"
/number=2
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/gene="MCP-1"
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complement (41846 . 41956)
/rpt family="purine-rich"
complement (42486 . .42569)
/rpt family="MLTII"
42979 . .43098
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                                                                                                                                                                                                                                                                              /rpt_family="MERSA"
complement(11031. 11072)
/rpt_family="MIR"
11567. 11834
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26135. 26228
/rpt_family="LTR16A"
complement (27814. .27950)
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28930. .28968
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complement(16483. 16653)
/rpt_family="MIR"
16830. 16949
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complement(40810, .4080p)
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|1293. .41469
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19362. .39414
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| rpt family="MER9"
| complement(12983. .13257)
| rpt_family="AluJb"
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24513. .25245
/rpt family="HERVL"
25613. .25758
                                                                                                                                                                                           /rpt_family="AT_rich"
8871. .8986
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17203. .17380
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17393. .18306
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18315. .24307
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/rpt_family="AT_rich"
complement(40152. .404
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9960. .30341
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32601. .32902
/rpt_family="AluSx"
complement(33593. .35
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/rpt_family="LIME3"
8023. .8048
                         /rpt_family="MLT1D" 7119. 73.67
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2364. .32581
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7689. .7888
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4309. .24335
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[0109. .10258
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2501. .12981
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Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maldrim, J., Molla, M., Morris, W., Morrow, J., Wychaleckyj, J., Nahle, R., Naylor, J., Nileg, W., McConnor, T., O'Donnell, P., Stange-Thoman, N., Stilwall, J., Stojanovic, N., Stone, C., Stange-Thoman, N., Stilwall, J., Stojanovic, N., Stone, C., Stange-Thoman, N., Stilwall, J., Stojanovic, N., Stone, C., Vassiliev, H., Vo, A., Magner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.

Loubmitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, J. Charles Street, Cambridge, MA 02141, USA
Research, J. Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Cearny, J., Colangelo, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Rourest, C., Punke, R., Gage, D., Carliss, D., Depayre, E., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Madonald, P., Marton, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marton, L., Morrow, J., Mychalecky, J., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Matheler, J., Noberts, D., Roy, A., Wagner, M., Morris, M., Morrow, J., Mychalecky, J., Nahf, R., Nalley, M., Metley, N., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyasillev, H., Vo, A., Wagner, A., Wheeler, J., Wheeler, J., Wu, Y., Wyasillev, H., Wo, A., Wagner, A., Wheeler, J., Wheeler, C., Mult, Y., Wo, A., Wagner, A., Wheeler, C., Mult, Y., Whan, D., Stolanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, H., Vo, A., Wagner, A., Wheeler, C., Mult, Y., Wo, A., Wagner, A., Wheeler, C., Mult, Y., Wo, A., Wagner, M., Wheeler, C., Mult, Y., Wo, A., Wagner, M., Wheeler, C., Mult, Y., Wo, A., Wagner, M., Wheeler, C., Mult, Y., Wo, A., Wagner, M., 
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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rpt_family="MIR"
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/rpt_family="MER81"
5131 6250
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1980. .3131
'rpt_family="MER5A"
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ACC21222 177426 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome 11 clone RP11-567M21, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
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Direct Submission
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
ON May 12, 2000 this sequence version replaced gi:7233676.
             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177426)
Waterston, R.H.
                                                                     GAAGCCCAGAACTCTCTGATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
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1144: gap of unknown length
2529: contig of 1385 bp in length
2629: gap of unknown length
3739: contig of 1110 bp in length
3839: gap of unknown length
5188: contig of 1349 bp in length
    178 ATAAAAATGCAGACTGTGATTCAGCAGGTCTGGGTT
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Unpublished
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO SADIENS (human)
HOMO SADIENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGAGTTGAAGCCCCAGAACTCTCTGATAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AATGCCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
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                                                                                                                                                                                                       Length 147416;
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Best Local Similarity 100.0%; Pred. No. 2.9e-76;
Matches 300; Conservative 0; Mismatches 0;
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other sequences; artificial sequences.
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Sequence 1625 from Patent WO0200928.
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                                                                                  / Complement (47075. 47140)
/ rpt family="MLTIG"
complement (47266. 47307)
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complement (47363. 47442)
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complement (48165. 48209)
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complement(47075.
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5288: gap of unknown 6861: contig of 1573 6961: gap of unknown 8387: contig of 1426 8487: gap of unknown	9957: contig of 1470 10057: gap of unknown 11934: contig of 1877 12034: gap of unknown 15639: contig of 3605 15739: gap of unknown 18805: contig of 3065	18905: contig of 2000 21750: contig of 2845 21850: gap of unknown 24673: contig of 2825 24773: gap of unknown 27874: contig of 3101 27974: gap of unknown 32401: contig of 4427 32501: gap of unknown 35859: contig of 3358	38608: contig of 2649 38708: gap of unknown 43983: contig of 5275 44083: gap of unknown 50370: contig of 6287 50470: gap of unknown 55419: contig of 64949 55519: gap of unknown 60146: contig of 4627 60246: gap of unknown 6590: contig of 4627	* 65991 66090: gap of unknown 66091 72510 72519: contig of 6429 72520 72619: gap of unknown 72620 7368: contig of 6749 7368: gap of unknown 79469 8631: contig of 9163 88732 88731: gap of unknown 88732 98171: contig of 9440 88732 98271: gap of unknown 98272 108874: contig of 108075 1108974: gap of unknown 120957 120956: contig of 1188 120957 133832: contig of 1240957 133832: contig of 1240957 133832: contig of 1240957 133832: contig of 1240957 133832: contig of 1240957 133832: contig of 1240957 133833 1531337: contig of 1240957 154437: gap of unknown 151338 151437: gap of unknown 151338 151437: gap of unknown 151338 174426: contig of 2598	cation/Qualifier: 177426 177426 177426 177426 1 type="genomic bxref="taxon:96" hromosome="11" 100e="RP11-567M2. 1044 45. 2529 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar 0te="assembly_nar

100140 AAAATACAAAAATTAGCCAGGTGTGATGGCATGTGACTGTAGTCCCAGCTACTAGGGAGG 100081 ö 61 CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120 9 1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG Gaps .; 0 Query Match 54.7%; Score 164; DB 2; Length 177426; Best Local Similarity 84.1%; Pred. No. 9e-37; Matches 185; Conservative 0; Mismatches 35; Indels 0; 99960 AAAAAAAAAAAGAATGCTAAGCAAACAAGGCATGGTGGC 99921 181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCC 220 24774. .27874 /note="assembly\_name:Contig24" 27975. .3340! /note="assembly\_name:Contig25" 32502. .35859 clone end: 77
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                                                                                                                                                                    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA to bulished Only in Database (2000)

La (bases 1 to 188172)

R Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

L Submitted (11-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

L-22 Suchiro-chou,Tsurumi-Vu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-84-503-911, Fax:81-45-503-9170)

On Aug 9, 2002 this sequence version replaced gi:20334333.
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Homo sapiens genomic DNA, chromosome 11 clone:RPI1-567M21, complete
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1 (bases 1 to 238472)

DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                              Chordata, Craniata, Vertebrata, Euteleostomi,
Primates; Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 5 clone CTB-125B20, complete sequence.
AC010290
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Pred. No. 9e-37;
0; Mismatches 35; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
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/clone="RP11-567M21"
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2 (bases 1 to 238472)
DOE Joint Genome Institute.
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Mammalia; Eutheria;
                                                                                                   Homo sapiens (human)
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Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 238472)

SS DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

AL Submitted (23-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Oct 23, 2001 this sequence version replaced gi:7711412.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.7% of Sequence;

Estimated Total Number of Errors is 0.5.

Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers
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On Mar 7, 1999 this sequence oversion replaced gi:4056528.

On Mar 7, 1999 this sequence eversion replaced gi:4056528.

Where differences are found these are annotated as variations where differences are found these are annotated as variations variation may not be found in the sequence submission variation on anotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession
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Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1
Contains the SLC2A10 gene encoding a solute carrier family 2
(facilitated glucose transporter) member 10, the 5' end of a novel
gene, BSTs, STSs, GSSs and three CpG islands, complete sequence.
AL031055.1 GI:4375937
HTG; CpG island; SLC2A10.
Homo sapiens (human)
Homo sapiens (human)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 9.1e-37;
0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Ramsay, H.
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ilarity 84.1%;
Conservative
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3963. .5655

//note="L1MAB repeat: matches 4532. .6270 of consensus"

569. .5895

/note="L1ME repeat: matches 5501. .5739 of consensus"

6332. .6548

/note="L2_repeat: matches 2524. .2746 of consensus"
                                                                                                                                         .391 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="LTR16C repeat: matches 126, .316 of consensus"
0631, .10690
note="MLT1D repeat: matches 445, .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8685. 8793
/note="Milly repeat: matches 271. .366 of consensus"
9095. .9221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MLTID repeat: matches 128. .192 of consensus"
1762. .12062
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3660. .13783
note="LTR33 repeat: matches 330. .452 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5774. .15952
/note="MERS8A repeat: matches 42. .220 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864. .7934
note="MLT1I repeat: matches 311. .382 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluJo repeat: matches 74. .306 of consensus"
.0038. .10206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7323. .7417
"note="L2 repeat: matches 2389. .2513 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2303 of consensus"
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/note="L2 repeat: matches 2657. .2744 of consensus"
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note="MIR repeat: matches 102. .242 of consensus"
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100ce="MiTID repeat: matches 1. .128 of consensus"

complement (12181. .12344)

/note=match: GSS: Em:AQ190762"

13011. .13129
                                                                                                                                                                                                                                                                                                                                                                                  .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .312 of consensus"
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/note="AluSq repeat: matches 1. .300 of consensus"
8685. .8793
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864. .7934
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| note="MSTB repeat: matches 2. .409 of consensus"
| 11670. .11761
                                                                                                                                                                                                                                                                                                                                                                                                                                           .62 of consensus"
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'note="4 copies 20 mer 76% conserved"
5476. .15752
                                                                                                            1865. .3962
/note="MER21B repeat: matches 299.
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/note="MLT1J repeat: matches 9.
8347. .8647
                                                                                                                                                                                                                                                                                                                                              6626. .6915
/note==#Allusx repeat: matches 3.
6918. .6980
/note==#RER94 repeat: matches 1.
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/note="AluJo repeat: matches 1.
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note="L2 repeat: matches 2170.
                                                                         note="match: STS: Em:G15621"
                                                   gene="dJ101A2
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/note="MER20 re
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.5774. .15952
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numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence
vas generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RPI-28H20 This sequence
was finished as follows unless otherwise noted: all regions were
cither double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assembly
was confirmed by restriction digser. RPI-28H20 is from the library
Apt.il one tructed by the group of Pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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/note="AluSx repeat: matches 1. .298 of consensus"
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'note="MIR repeat: matches 50. 151 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .262 of consensus"
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note="MIR repeat: matches 8. 135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(<1. .562,2463.
/gene="dJ101A2.2"
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'note="MIR repeat: matches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 2248
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us-09-899-276c-6.rge

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                                                                                                                                                                                                                                                     Cosmid R27090 overlaps cosmid R32469 to the left and cosmid R31317 to the right.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="mpsilon- COP"
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/note="clathrin -ordered protein; Identified through
sequence homology to epsilon-COP product from C.griseus
sequence homology to epsilon-COP product from (griseus
(87% identity; Z32554) and B. taurus (89% identity;
X76980).
                                                                                     Liamerdin, J.E.
Direct Submission
Submitted (12-0CT-1997) Human Genome Center, Lawrence Livermore Nubmitted (20-0CT-1997) Human Genome Center, Capter National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere.
Submitted (29-SEP-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA 3 (bases 1 to 38041)
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9272. .10204
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8300. .847
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723_ Roor
                                                                                                                                                                                                                                                                                                                                                                                      l. .38041
′organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
complement(2762...
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'rpt_family="Alu"
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complement(7998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="R27090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1671
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                                                                                                                 AUTHORS
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                      JOURNAL
                                                                              REFERENCE
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1 (Dases I to 3804).

1 (Dases I to 3804).

1 (Dases I. To 3804).

Garcia, E., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC002985 38041 bp DNA linear PRI 22-OCT-1997
Human DNA from chromosome 19-specific cosmid R27090, genomic
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16804. .17190
/note="WER57B repeat: matches 1. .403 of consensus"
17198. .17297
                                                                                                                                                                                                                                                                                                                                                //occe="47".
//notce="AluSx repeat: matches 1. .312 of consensus"
17939. .18240
//notce="LTR26 repeat: matches 246. .553 of consensus"
complement(18333. .18408)
//notce="match: STS: Em:G42885"
18451. .18615
//notce="PAM repeat: matches -126. .41 of consensus"
19258. .19336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGGCAGGAGAACCTTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAAAATAGTGC
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'note="MER57-internal repeat: matches 7168. .7244 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19343. .19485

... ote-"MRES" repeat: matches 2. .180 of consensus"

19721. .20190

/note-"LTR8 repeat: matches 251. .691 of consensus"

20238. .20493
                                                                                                                 .2657 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluJb repeat: matches 1. .296 of consensus"
16600. .16635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 127418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                    note="5 copies 20 mer 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 163.4; DB 9
Pred. No. 1.3e-36;
                                                                                                           /note="L2 repeat: matches 2617.
16641. .16803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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2 (bases 1 to 38041)
Lamerdin, J.E.
Direct Submission
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ilarity 82.1%;
Conservative
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 188; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

TITLE

LOCUS

ACCESSION

AC002985/c

RESULT 9

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AEKRQEVKEAARLAREKSQDGGELTSPALGLASHQVSTPYSPMPAWAPVPPSPLVSAN
GPGEBELFRSGSADAPGPTBRERLKGVLSEGSVGBVQWBABFFFALQDSNNKLAGALRE
ANAAAQWRQQLEAQRAEAERLRQRVAELEAQAASETYTPTGEKEGLGGGGSLEQLEAL
VQTKOOGLOTICKSQTGSPREALEAARBEETQCKVQDLETRNAELEHQLRAMBRSLEEA
RAERBRARARVGRAAQLLDVSLFELSELREGLARLAEAAP"
('rpt. family="alu"
23231. .23507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27006
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                                                                                                                                                                       /trānslation="mSTAREQPIFSTRAHVFQIDPATKRNWIPAGKHALTVSYFYDAT
RNVYRIISIGGAKAIINSTVTPNMTFTKTSQKFGQWADSRANTVYGLGFASEQHLTQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC012094 80952 bp DNA linear HTG 08-JAN-2003 Homo sapiens chromosome 3 clone RP11-10315, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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I (bases I to 80952)
Muzny, D.M., Addams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Bankendurg, K., Bonnin, D., Barbaria, J., Benten, J., Balmage, K., Bankenburg, K., Bonnin, D., Buock, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27125 AAAATACAAAAATTAGCCAGGCGTGGTGGCATGCGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27065 craagacaagaarcacrraaacccagaaragaagarracagraargaagaccaagarcargc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
     Drosophila EST matches: AA391781, AA202338, AA201147,
AA202832,AA246370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 160.8; DB 9; Length
Pred. No. 7.3e-36;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
23533 . 24266
/rpt_family="Alu"
/rpt_family="Alu"
complement(26954 . 27247)
/rpt_family="Alu"
complement(27925 . 28084)
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement (28377. .28665)
/rpt family="Alu"
28980. .29921
                                                                                        /product="R27090_3"
/protein_id="AABB1545.1"
/db_xref="G1:2443871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26945 GAAATGGCTAAGTGTGAGGCAGAA 26922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAAATGCAGACTGTGATTCAGCA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28980. .29921
/rpt_family="Alu"
/s950. .30567
/rpt_family="Alu"
30657. .30931
/rpt_family="Alu"
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AC012094 AC01209
AC012094.16 GI:20279325
HTG, HTGS PHASE1.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%;
86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.8<sup>3</sup>
Matches 177; Conservative
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AC012094/c
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// note="BLASTN similarity to 241188 (1. 67); match: 0.94, score: 8.58-89; database searched: est; H. sapiens partial cDNA sequence"

complement (join(22685. 22876,24567. 24653,24751. 24867, 25218. 23374,4866. 26287,27566. 27652,31595. 31726, 31970. 32126,32211. 33224)

// note="Hypothetical 41.3 kDa human protein most similar to Vesl and GLGF proteins of rat; Residues 1-128 of hypothetical protein 827090 are 81% identical to Rat GLGF protein (402079) and 83% identical to Rat Vesl protein (1092079) and 83% identical to Rat Vesl protein (AB003726), both proteins are expressed in brain and upregulated during seizures.

Human EST matches: M42820, AA121538, W42730, AA127702

MOUSE EST matches: AA407944, AA408331, AA013888, AA035853, AA212542
                                                                                                                                                                                           join[12984]. 13098,13822. 13945,14905. 14990,15085. 15206,
15568. 15755,15846. 15986,17475. 17550,17865. 17941,
18124. 18221,19545. 19619,21008. 21096,21207. 21278,
                                                                                                                                                                                                                                                                        21370. .21558)
/ note="Hypochetical 56kDa human ATP-dependent RNA helicase; Putative ATP-dependent RNA helicase of DEAD box family. Most similar (57% identical) to probable ATP-dependent RNA helicase Dbp45A (538329) - fruit fly (Drosophilar melanogaster)
Human EST matches: AA34472, H08289, AA464032, AA196836, AA559862, AA573466, AA464741, W46150, AA535538, AA488261, W46162, R00974, AA378518, R26194, R15246, AA359638, etc. Mouse EST matches: AA271508
Drosophila EST matches: AA271508
Rat EST match: H35240"
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0.85, score: 3.5e-33; database searched: est; H. sapiens
partial cDNA sequence"
complement (21611. 21871)
/note="BiASTN similarity to T16014 (1. 261); match: 0.94,
score: 1.1e-90; database searched: est; IB2449 Infant
brain, Bento Soares Homo sapiens cDNA 3'end."
complement (21615. 21825)
/note="BiASTN similarity to Z41188 (42. 252); match: 0.92,
score: 8.5e-89; database searched: est; H. sapiens partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / trainiation="MAGFAELGLSSWLVBQCRQLGLKOPTPVQLGCIPALLEGRDCLG
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IT GGROWVAQALELSRKPHVIATPGRIADHLRSSNTFSIKKIRFLWWDEADFLLEQ
GCTDFTVDLEAYLAAVPRRRQTLFSATLTDTLRELQGLATNOPFFWEAQAPVSTVED
LDQRYLLVPEKVKDAYLWHLIQRFQDEHEDWSIIIFTNTCKTCQILCMMLRKFSFPTV
ALMSWMCKQRYRRRAALAKFKSSIYRILATDVARGLDIPTVOVVINHWPTGLPKYYIH
RVGRTRAAGRQCQATTLUYQYDIHLYMAIEEDIKKKLEEFSVEEAEVLQILTQVNVVW
RECEIKLEAAHFDEKKEINKRKQLILEGKDPDLEAKRKAELEXIKQKNRRFKEKVEET
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complement (11721. .11961)
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join(12984. .13098,13822. .
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/rpt family="Alu"

complement (17052. 17340)

/rpt family="Alu"

18380. 18802
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cuelland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Devila, M.L., David, C., David, D.B., Din, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Dinn, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Dinn, Y., Dinh, H.H., Delaney, K.G., Elbaj, C., Ecotto, M., Farigar, D., Fraggy, N., Ford, J., Foster, P., Frantz, P., Farraguco, D., Riagg, N., Ford, J., Foster, P., Frantz, P., Harris, C., Harris, K., Hart, M., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgon, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Howard, S., Huber, J., Huly, S., Hume, J., Jonson, B., Garzon, S., Huber, J., Huly, S., Hume, J., Jonson, B., Garzon, S., Karlsson, E., Rallson, R., Karlson, E., Rantson, E., Rantson, E., Rantson, R., Kan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Rantson, R., Manter, G., Martin, R., Martin, R., Ma, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulsegdd, H., Lozado, R.J., Lux, Lucier, R., Luna, R., Ma, J., Martin, R., Mahler, G., Martin, R., Martin, R., Martin, R., Mantine, R., Manter, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Moren, M., Nickerson, E., Nuckend, M.P., Meador, M., Morgan, R., Nickerson, E., Nuckend, M.P., Martin, R., Ren, Y., Retves, M., Nolle, R., Ren, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Weinston, M., Weinston, M., Weinston, M., Weinston, M., Weinston, M., Weinston, M., Weinst
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Center: College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hggc-hellp@bcm.tmc.edu
Contact: hggc-hellp@bcm.tmc.edu
Contact: project Information
Center project name: HTM110
Center clone name: RF11-10315
Center clone name: RF11-10315
Center clone name: RF11-10315
Contact: bgc-herminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 62640 bases at least Q40
Consensus quality: 75786 bases at least Q30
Consensus quality: 75786 bases at least Q30
Consensus quality: 75786 bases at least Q30
Estimated insert size: 102946; squarose-fp estimation
Estimated insert size: 182186; squarose-fp estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 80952)
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Direct Submission
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COMMENT

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61 CTGAGGCAGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
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consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Best Local Similarity 89.6%; Pred. No. 1.3e-35;
Matches 172; Conservative 0; Mismatches 20; Indels 0
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628 65727: gap of unknown 14
728 73013: contig of 7286 bj
714 73113: gap of unknown 14
114 80952: contig of 7839 bj
Location/Qualifiers
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gap of unknown 1
contig of 2001 b
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                                                                                                                                                                                                      Submitted (30-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 21, 1999 this sequence version replaced gi:3603098.
                                                                                                        PRI 30-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ali,J., Elliott,G., Le,T. and Wohldmann,P.
The sequence of Homo sapiens BAC clone RP11-84K19
Watersten,R.H.
Submitted (15-SEP-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Materston,R.H.
A (bases 1 to 162139)
Waterston,R.H.
Submitted (15-SEP-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Materston,R.H.
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Submitted (07-027-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
( Dases 1 to 162139)
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                               ACO05682 162139 bp DNA linear PRI 30-J
Homo sapiens BAC clone RP11-84K19 from 7, complete sequence.
AC005682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
                                                                                                                                                   AC005682.2 GI:5757537
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                              AAATATATACAC 47739
                                                                                                                                                                               Homo sapiens (human)
181 AAAATGCAGAC 192
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                                                                        RESULT
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DRIK/GFP/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is RP11-319F3. Actual start of this clone is at base position 52619 of RP11-319F3 actual end is at base position 16219 of RP11-84K19.

Location/Qualifiers
                                                                                            NOTICE: This sequence may not represent the entire insert of this form. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
Center project name: H_NH0084K19
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/chromosome="7"
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/rpt_family="AT_rich"
794. .1013
/rpt_family="Alu"
1016. .1218
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100. .207
/rpt_family="L2"
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/rpt_family="Alu"
2765. .23657
/gene="DRCTNNB1A"
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1659. .1702
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1267. .1330
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1399. .1657
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1822. .2049
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2137. .2441
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Submitted (20-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Numquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

Numquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Well. WORMPEP; Information on the WORMPEP there is no and the beautiff of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the parameter of the par
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                               AL445685 142790 bp DNA linear PRI 21-APR-2002
Human DNA sequence from clone RP11-91A18 on chromosome 1, complete
sequence.
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     Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 77.5%; Pred. No. 1.9e-35;
Matches 193; Conservative 0; Mismatches 56
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AL445685.18 GI:20302179
                                                                                                                                                                  96082 AAATATATACAC 96071
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                                                                                                                     181 AAAAATGCAGAC 192
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                                                                                                                                                                                                                                                                                 /product="unknown"
/product="unknown"
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DLAQKALDDIIYRAQLELYPEPLLVANAIKASLPHGPMKSNKEGTRCIQVETTPTSSR
ISRNAYTSAGISKGHRWKRHGAYTBLTGQSELMEISBYDGGFYSRAASSTSGSGLSNSSH
ISRNAYTSAGISKGKKKETTGGSCKDHFARKQTQRAQSBNLELLSLKRLI
INTSQSLPKDSSHGAKTAATVFSKSFRQVSGYTVPHNPSSAVGCGAGTDANRFSACS
LQEEKLIYVSERTELPMKHQSGQQRPPSISITLSTD"
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.23657)
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                                                                                          join(<2765. .2881,5974. .6061,6881. .7040,21133. /gene="DRCTNNB1A"
/note="Homo saplens down-regulated by Ctnnb1, a (DRCTNNB1A), mRNA.; H NH0084K19.1
This gene was based on gi(14211900 17511708)
                                                                                                     .7040,21133.
oin(2765. .2881,5974. .6061,6881. .7040,21133.
                                               .7040,21133.
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                       gene="DRCTNNBIA"
|oin(2765. 2881,5974. 6061,6881.
|gene="DRCTNNBIA"
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16837 ...1772
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5403...5469
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6225..6528
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/rpt_family="Alu"
/rpt_family="Alu"
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9242 ... 9365

/rpt_family="AT_rich"

9809 ... 9910

/rpt_family="T_rich"

10509 ... 10654
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/rpt_family="AT_rich"
18739. .18911
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3035. .13081
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4679. .15246
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18163. .18190
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1276. .11366
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7930. .18132
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2380<u>6</u>.
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Pan troglodytes (chimpanzee)

Pan troglodytes

Pan troglodytes

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (bases 1 to 208066)

Trani,L., Cotton,M., Haglund,K. and Bielicki,L.

The sequence of Pan troglodytes BAC clone RP43-30K12

Unpublished (2001)

S Suleton,J.E. and Wilson,R.

S Squencing of Pan troglodytes

L (bases 1 to 208066)

S Uleton,J.E. and Wilson,R.

S Gauencing of Pan troglodytes

L Unpublished (2001)

E 3 (bases 1 to 208066)
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, Clint', Yerkes #C0401; birthdate: 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at
              Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
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Pan troglodytes BAC clone RP43-30Kl2 from 7, complete sequence.
AC146483
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128996. .129012
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Pred. No. 5.7e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/chromosome="7"
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128925. .128976
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .190149
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  MAPPING INFORMATION:
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Matches 168; Conservative
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AC146483
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                          PRI 09-JUN-2004
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1 (bases 1 to 190149)

Trani,L., Haglund,K. and Meyer,R.

The sequence of Pan troglodytes BAC clone RP43-23F10

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.K.
Direct Submission
Submitted (27-APR-2004) Genetics, Genome Sequencing Center, 4444
Forest Park Warkway, St. Louis, MO 63108, USA
4 (bases 1 to 190149)
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Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 190149)
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Pan troglodytes BAC clone RP43-23F10 from 7, complete sequence.
AC146127
CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                          Genetics, Genome Sequencing Center,
Louis, MO 63108, USA
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On Jun 2, 2004 this sequence version replaced gi:46576149.
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Submitted (02-JUN-2004) Ger
Forest Park Parkway, St. L.
5 (bases 1 to 190149)
Wilson, R.K.
Direct Submission
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Submitted (03-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Dec 21, 2003 this sequence version replaced gi:33386957.
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                                                                                                                                                                                                                                                                                                                                     PRI 03-JAN-2004
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 211780)
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USA
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Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 211780)
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Pan troglodytes BAC clone RP43-165A19 from 7, complete sequence.
AC146006
                                                                                       Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trani, L., Cotton, M. and Haakenson, W.
The sequence of Pan troglodytes BAC clone RP43-165A19
Unpublished (2001)
2 (bases 1 to 211780)
Wilson, R.
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Submitted (23-AUG-2003) Genetics, Genome Eubmitted (23-RWay, St. Louis, MO 63108,
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Contact: submissions@watson.wustl.edu
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Submitted (21-DEC-2003) Genetics, Genome S
Forest Park Parkway, St. Louis, MO 63108,
6 (bases 1 to 211780)
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Pan troglodytes
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5 (bases 1 to 211780)
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                                                                                                                                                                                                                                         Direct Submission
Submitted (29-OCT-2003) Department of Genetics, Washington
Submitted (29-OCT-2003) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 4, 2003 this sequence version replaced gi:33859971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                         Direct Submission
Submitted (19-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 208066)
                                                                                                                                               Submitted (04-OCT-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 208066)
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    .349
    /note="Sequence derived from one plasmid subclone."

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Pred. No. 5.7e-35;
0; Mismatches 17; Indels 0; C
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                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .208066
forganism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="laxon:9598"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: C_PT030K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP43-30K12"
/clone lib="RPCI-43"
1. .349
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http://www.bacpac.chori.org.
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                                                                                                            Wilson, R.K.
Direct Submission
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Best Local Similarity
Matches 168; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                     AUTHORS
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                                                                                              REFERENCE
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restriction digest

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169993 AAAATACAAAATTAGCCCGGTGTGGTGGCCATGTGCCTGTAATCCCAGCTACTCCGGGAGG 169934
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Clint', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.
                  Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
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Anote="Sequence derived from one plasmid subclone."
143326. .143405
/note="Sequence derived from PCR product of project DNA."
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This sequence is the entire insert of the clone. This clone is
overlapped by AC146236.
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/note="Sequence derived from one plasmid subclone."
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/note="Sequence derived from one plasmid subclone."
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="7"
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/clone_lib="RPCI-43"
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1. .211780
MAPPING INFORMATION:
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Best Local Similarity 90.8'
Matches 168; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

8780412 Total number of hits satisfying chosen parameters:

4390206 segs, 2959870667 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2004as:\*geneseqn2004bs:\* geneseqn2003cs:\* geneseqn2003ds: geneseqn2003as:\* geneseqn2003bs:\* N Geneseg 16Dec04:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn1980s:\* geneseqn1990s:\* :01 11: 12: 13: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Ouerv Result 0000 υ

Description	Adh13943 Human mon	Ado03803 Human Cc1	Abl33652 Human imm	Aak67211 Human imm	Abd33528 Human can	Abk42328 Genomic s	Abk42327 Genomic B	Adb60483 Connectiv	Adb60484 Connectiv	Abk69846 Human sec	Acc50861 Human sec	Abz71483 Secreted	Adb91839 Human sec	Adc74614 Human sec	Add38134 cDNA clon	Ada57728 BAC fragm	Aak72318 Human imm	Abk69845 Human sec	Acc50860 Human sec	Abz71482 Secreted	
ID	ADH13943	AD003803	ABL33652	AAK67211	ABD33528	ABK42328	ABK42327	ADB60483	ADB60484	ABK69846	ACC50861	ABZ71483	ADB91839	ADC74614	ADD38134	ADA57728	AAK72318	ABK69845	ACC50860	ABZ71482	
DB	9	12	9	4	13	4	4	σ	σ	9	œ	œ	σ	10	10	10	4	9	<b>c</b> o	œ	
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Match	0.00	100.0	5.9	3.6	3.6	7.7	2.1	2.1	2.1	7.7	52.1	52.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	
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Score	300	300	167.8	160.8	160.8	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	156.4	
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Adb91838 Human sec	Adc74613 Human sec	Add38133 cDNA clon	Adas7727 BAC fragm	Adq20606 Human sof	Abd32694 Human can	Aak81320 Human imm	Adc87623 Human GPC	Adc87010 Human GPC	Abz74262 Secreted	Ada98791 Human sec	Abz67828 Human sec	Acn44898 Human gen	Abd32581 Human can	Abn96931 Gene #342	Continuation (3 of	Abk83567 Human cDN	Aal54074 Human tra	Adq59422 Human can	Adp45592 Human MAP	Acn44958 Human gen	Adf77178 KALPA gen	Acn44298 Human gen	Aal02649 Human rep	Aba07691 Human ova
ADB91838	ADC74613	ADD38133	ADA57727	ADQ20606	ABD32694	AAK81320	ADC87623	ADC87010	ABZ74262	ADA98791	ABZ67828	ACN44898	ABD32581	ABN96931	ACH03408 2	ABK83567	AAL54074	ADQ59422	ADP45592	ACN44958	ADF77178	ACN44298	AAL02649	ABA07691
σ	10	10	10	12	13	4	10	10	œ	œ	10	1	13	ø	σ	9	10	12	12	11	10	1	4	4
20245	20245	20245	20245	195917	252907	5021	118584	349999	232	232	232	144723	83517	99014	110000	112460	197997	246940	76500	285020	86131	114615	499	499
52.1	52.1	52.1	52.1	51.9	51.8	51.5	51.3	51.3	51.2	51.2	51.2	51.0	50.9	50.9	50.9	50.9	50.6	50.5	50.5	50.5	50.4	50.4	50.3	50.3
156.4	156.4	156.4	156.4	155.8	155.4	154.6	153.8	153.8	153.6	153.6	153.6	153	152.8	152.8	152.8	152.8	151.8	151.6	151.4	151.4	151.2	151.2	151	151
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## ALIGNMENTS

Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:6. ADH13943 standard; DNA; 300 BP 11-MAR-2004 (first entry) ADH13943; RESULT 1 ADH13943

ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma.

06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. EP1170372-A1. 09-JAN-2002. 

Homo sapiens,

Poustka A; Delius H, Finzer P, Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A;

WPI; 2002-165895/22.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. Disclosure; SEQ ID NO 6; 30pp; English. The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention mas cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

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EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to
                                                                                                                                            9
pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                      AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCCAGAACTCTCTGATAAATTC
                                                                                                                                                                                                                                                                           AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCCAGAACTCTGTGATAAATTC
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                                                                                                                                           AAAATATAAAAATTAGCCAGGCCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                   CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                                                                                                                                             AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testing candidate drug for treating age-related macular degenera administering drug to Cc12-deficient, Ccr2-deficient knockout mc analyzing development or regression of drusen and/or lipofuscin
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0
                                                                              Length 300;
                                                                                                    Indels
                                                          Sequence 300 BP; 95 A; 60 C; 76 G; 69 T; 0 U; 0 Other;
                                                                              Score 300; DB 6;
Pred. No. 1.8e-77;
0; Mismatches 0;
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ilarity 100.0%;
Conservative 0
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                                                                                           Similarity
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Matches 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antianaemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiartic; antiatheumatic; antiatic; antidiabetic; antiportatic; antinflammatory, cancer; eye disease; arteriosclerosis; anematory, cancer; eye disease; arteriosclerosis; anematory, remover, sy disease; AIDS; epilepsy; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
administering a candidate drug to gene knockout mice, in particular Cc1 deficient, Ccr2-deficient and/ or a Cc12-deficient(Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities can be used for gene therapy purposes. This polynucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crigagecadeagaactrcrrgaarccaggaggcgcaggrrgcagrgaggagagaragrgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2620 CACTGCACTCCAGCTGGGTGACAGAGTGAGACTCTGTCTCAAAAAATAAAATAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAIGCAGACIGIGAIICAGCAGGICIGGGIIIGAAGCCCCAGAACICCIGAIAAAIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAATATAAAAATTAAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                    Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                  Score 300; DB 12;
Pred. No. 7.3e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 7.3
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        100.08;
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2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 300; Conservative
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2000US-0225758P.
2000US-0225759P.
2000US-0226279P.
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2000US-0225213P.
2000US-0225214P.
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2000US-0225267P.
2000US-0225268P.
                                          2000US-0217487P
                                                        2000US-0217496P
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2000US-0225447P.
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2000US-0230437P.
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2000US-0232401P.
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2000US-0234998P.
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20-OCT-2000; 2000US-0241786P
                                                                                                       14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
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02-OCT-2000;
02-OCT-2000;
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12-SEP-2000;
14-SEP-2000;
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22-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEP-2000
    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                        58 AGGCTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGAGATAG 117
                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                         ATAAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCAGAACTCTCTGATAAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICAATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTAC 297
                                                                                                                                                                                                                                                                                                   1 AGGTTGAGGTAGGAGAATTTTTGAATTTTAGGAGGCGTAGGTTGTAGTGAGTAGAGATAG 60
Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                  including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTAATGGTATTTAATTATTTGGAGGTTATGGATGTTTTGTTAATAGAAGTTAT
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22023
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                                                                                                                                                                                                                                 Length 5926;
                                                                                                                                                                                                       Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                      Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                              Score 167.8; DB 6;
Pred. No. 2.2e-38;
0; Mismatches 47;
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ID AAK67211 standard; DNA; 12026 BP.
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2000US-018464P.
2000US-0186350P.
2000US-0190076P.
2000US-0190076P.
2000US-019123P.
2000US-0205515P.
2000US-0205515P.
                                                                                                                                                                                                                                55.9%;
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                                                                                                                                                                                                                              Query Match 55.9
Best Local Similarity 80.7
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGA 300
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18-APR-2000;
19-MAY-2000;
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24-FEB-2000;
02-MAR-2000;
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28-JUN-2000;
                            methylation.
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120

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0; Gaps

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The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer
supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK6764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAW82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4683 AAAATACAAAAATTAGCCAGGCGGGGGGGGGGGGGGGGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAGGCAGGAGCACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAATAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                        Sequence 12026 BP; 2791 A; 3406 C; 3411 G; 2418 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             53.6%; Score 160.8; DB 4; Length 12026; 86.8%; Pred. No. 3.1e-36; ive 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer-associated (CA) gene HD07-104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4503 GAAATGCCTAAGTCTGAGGCAGAA 4480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AAAAATGCAGACTGTGATTCAGCA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD33528 standard; DNA; 31926
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; cancer; cytostatic
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Matches 177; Conserv
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    17249 AAAATACAAAAATTAGCCAGGCGTGGTGGCATGCGCCTGTAGTCCCCAGCTACTCGGGAGG 17308
                                                                                                                                                                                                                                                    drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                 Genomic sequence #227 encoding novel human connective tissue polypeptide
                                                                                                                                                                                             AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                     CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                                                                                                      0; Gaps
                                                                                                                        Sequence 31926 BP; 6797 A; 9017 C; 8858 G; 7254 T; 0 U; 0 Other;
                                                                                                                                               DB 13; Length 31926;
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                                                                                                                                             53.6%; Score 160.8; DB 1
86.8%; Pred. No. 4.5e-36;
tive 0; Mismatches 27
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                                                                                                                                            Query Match
Best Local Similarity 86.8
Matches 177; Conservative
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02-MAR-2000;
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The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leic acid encoding novel connective tissue associated polypeptides, ed in diagnosing, preventing, treating or ameliorating a disorder such cancer or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5304 BP; 1550 A; 1037 C; 1017 G; 1700 T; 0 U; 0 Other;
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         2000US-0246478P.
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                                                                                                                            Genomic sequence #226 encoding novel human connective tissue polypeptide.
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           Gaps
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cytostatic; gene; ds.
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  Pred. No. 4.4e-35;
0; Mismatches 41;
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02-MAR-2000; 2000US-0184664P.
17-MAR-2000; 2000US-0199076P.
18-APR-2000; 2000US-0199076P.
19-MAY-2000; 2000US-0198123P.
07-JUN-2000; 2000US-0205515P.
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                                              3450 AAAGAAGAAGAAGAAGAAGAGCTGTCTGGTCAAGGCCA 3409
                  181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGGTTGAAGCCCA 222
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antiarteriosclerotic; immunosuppressive; antirhaumatic; darmatchritic; antiarteriosclerotic; immunosuppressive; antirhaumatic; darmatchritic; antiaflammatory; antiaflargic; antiasthmatic; darmatchoical; mophrotopic; vincide; fungicide; antibacterial; antiparastic; antiparastic; antibacterial; antiparastic; systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer; cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder; Malzheimer's disease; Parkinson's disease; cardiovascular disease; whatherosclerosis; myocarditis; cardiopulmonary bypass complication; antipinitis; cardiopulmonary bypass complication; whitisis; cardiopulmonary bowel disease; nephritis; organ transplant rejection; immune system disorder; Bruton's disease; X-linked lymphoproliferative syndrome; MB-cell lymphoproliferative disorder; HIV; AIDS; infection; chromosome identification; chromosome mapping; connective tissue related polynucleotide; gene; ds.
   3570 CTGAGGCAGAAGAATCGCTTAAACCCGGGAGGCGGAGATTGCAGTGAGCTGAGATCATGC 3511
                               121 CACTGCACTCCAGCCTGGGTGACAGAGTGAGACTCTGTCTCAAAAAATAAAATAAAAATA 180
                                                             cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
                                                                                                                      3450 AAAGAAGAAGAAGAAGAAGGCTGTCTCGTCAAGGCCA 3409
                                                                                           181 AAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCA
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The polypeptide or polymuclectide is useful for preventing, treating, or meliorating medical conditions in a mammal. The connective tissue a polypeptides, polymucleotides and antibodies are particularly useful for treating, preventing and/or prognosing disorders of connective tissues (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus, celeroderma, or Sjogran's Syndrome), cancers, cancer metastases and/or neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, complications), autoimmune diseases (e.g. systemic lupus erythematosus, cheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            connective tissue-related polypeptides and polynucleotides, useful treating, preventing and/or prognosing e.g. disorders of connective sue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
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Barash SC; (HUMA-) HUMAN GENOME SCI INC Rosen CA, Ruben SM,

WPI; 2003-634869/60. P-PSDB; ADB59409.

New connective tissue-related polypeptides and polynucleotides, useful for treating, preventing and/or prognosing e.g. disorders of connective tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or neoplasias.

Disclosure, SEQ ID NO 1215; 248pp; English.

The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective tissue-related polymucleotide encoding connective tissue antigens (CTA). The polympetide or polymetheotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polympetides, polymucleotides and antibodies are particularly useful for proposing disorders of connective tissues treating, preventing and/or prognosing disorders of connective tissues treating, preventing and/or prognosing disorders (e.g. rheumatoid arthritis, disorid and systemic lupus erythematosus, selencema, or Siogren's syndrome), cancers, cancer metastases and/or neoplassias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

0; Gaps 52.1%; Score 156.4; DB 9; Length 5304; ilarity 81.5%; Pred. No. 4.4e-35; Conservative 0; Mismatches 41; Indels 0; Query Match Best Local Similarity Matches 181; Conservat

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(first entry)
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Matches 175; Conservative
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ACC50861
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                                                                                                                                          3630 AAACTATAAAAATTAGCTGGGCGTGGTAGCTGCCTGTAGTCCCAGCTACTCGGGAGG 3571
                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; secreted protein; gene therapy; immunosuppressive; antiarthuritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebroul ischaemia; angiogenesis; nervous system disorder; Albeimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector wector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or amelicate a medical condition in e.g. humans, mice, rabbits, goats, horses, cate, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR;
                                                                         Soppet
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Young PE,
                                                                                                                                                                                                                           AAAGAAGAAGAAGAAGAAGCTGTCTCTCGTCAAGGCCCA 3409
                                                                                                                                                                                          181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCA 222
                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein gene 22 genomic DNA fragment #7.
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Florence KA,
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Olsen H, Brewer LA, F,
Mucenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                    BP
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12-JAN-2001; 2001WO-US000911.
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disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arreef, cerebrovascular disorders e.g. cardiac arreef, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The presents ads DNA fragment of the gene for a novel human secreted protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; ss.
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es 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 156.4;
Pred. No. 5.5
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85.0%;
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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19-MAR-2002; 2002WO-US008276. 21-MAR-2001; 2001US-0277340P 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P.

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ABR48145) and their coding sequences (ACC50044-ACC50056). The proteins coding sequences (ACC50044-ACC50056). The proteins and their coding sequences (ACC50044-ACC50056). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary carteriosclerosis and myocardial isorders, reproductive disorders, immune system disorders, muscular disorders, pulmonary disorders, remained since disorders and for cancerous diseases and conditions, for proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treating or proliferation for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and parkinson's carecteristic thrombosis and with other disorders or neurodegenerative conditions such as Alzheimer's disease and parkinson's cransplants or bone and periodontal regeneration and aid in tissue cransplants or bone grafts, to prevent skin adjing or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marged in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of cembryonic stem cells, or to modulate mammalian characteristics or metabolism. The present sequence was used to illustrate the invention.

Compans before transplantation or for supporting cell culture of primary and is available from WIPO at companion or proliferation of former and is available from the present equence data for this patent was published in electronic former and is available from the companion or the companion or the companion or the companion or the companion or the companion or the companion or the companion or the companion or the companion or t
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                                                             invention relates to novel human secreted proteins (ABR47633.
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Disclosure; SEQ ID NO 1041; 1881pp; English.
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ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. protein genes, and ABP00011-ABP00299 represent the proteins they encode. CC invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant the use of the secreted proteins in drug screening, and recombinant covectors and host cells comprising a nucleic acid of the invention. The secreted proteins, uncleic acids encoding them, antibodies or antibody cradents specific for the secreted proteins, and modulators of protein crativity are useful for diagnosing, treating, ameliorating or preventing activity are useful for diagnosing, treating, ameliorating or preventing cospopagus, stomach, small intestine, large intestine, liver, biliary cospopagus, stomach, small intestine, large intestine, liver, biliary cract and pancreas, and include cancers of these organs and tissues. The reatment of immune disorders, inflammation, infection, cractment of immune disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome indentification, chromosome comping, in gene therapy, for identifying individuals from minute considering and protein genomic markers. The present sequence represents a human secreted protein genomic markers. The present sequence represents a human secreted protein genomic markers.
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                                                                                                                                                                                                                                                                                                                                                                                                                               New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1143-1145; 1216pp; English
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Best Local Similarity 85.0%;
Matches 175; Conservative (
                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM;
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoietic or haematologic disorder such as anaemia, autoimmune disorders such as rheunatoid arthritis, inflammation, Grave's disease, disbetes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including attention attention attention and hyperproliferative disorders including catherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene the polypeptide with a binding partner and determining whether the binding partner increases to decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5808 AAAATACAGAAAATTAGCTGGGTGTGATGGTGCGTGCCTGTAATCCCAGCTACTCGGGAGC 5867
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                                                       antidiabetic; immunosuppressive; dermatological; nephrotropic; antidaktineonian; neuroprotective; nootropic; antibacterial; virucide; fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic luqua srythematosus; glomerulonephritis; neurodegencative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
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Pred. No. 5.5e-35;
0; Mismatches 31; Indels 0;
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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85.0%;
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Best Local Similarity 85.0
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                      human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB91448 and ABB91815-ABB91911 encoding human secreted proteins ABB91449-
ABB91834. Also disclosed is a recombinant vector comprising a
ABB91834. Also disclosed is a recombinant vector comprising a
polynucleotide of the invention, and a recombinant host cell comprising
the recombinant vector. The polypeptide of the invention is useful in
identifying a binding partner by contacting the polypeptide with a
cleaning partner and determining whether the binding partner increases
of binding partner increases or
decreases activity of the polypeptide. The polypeptide, polynucleotide,
antibody or its fragment, agonist or antagonist are useful for preparing
antibody or its fragment, agonist or antagonist are useful for preparing
conditions related to diabetes. The present sequence is that of the human
immunoglobulin FC portion used to generate fusion proteins, increasing
the stability of the fused protein as compared to the secreted protein
conditions the sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding a human secreted protein is useful in diagnosing or treating diabetes or conditions related to diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to isolated nucleic acid molecules ADB91065.
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85.0%; Pred. No. 5.5e
tive 0; Mismatches
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-229407/22
                                                                               WO2003004622-A2
                             Homo sapiens.
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The present invention relates to an isolated polypeptide or human secreted protein. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind are useful for their fragments, and agonists or antagonists that bind are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders. The polypeptide is also useful for identifying a binding partner by contacting the polypeptide with a contact partner increases or decreases the activity of the polypeptide. The polypeptide and nucleic acid molecules are also useful for detecting, preventing, diagnosing, consplaying, treating or ameliorating inflammatory disorders or prognosticating, treating or ameliorating inflammatory disorders in explained in the polypeptide and disorders or gastrointestinal continuation, immune disorders, cardiovascular disorders, or gastrointestinal continuation, radiation hybrid mapping or long-range restriction disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction probes the polypeptides and antibodies are useful for providing combinate chemistry assays. The present sequence represents a cDNA clone for mapping is monohistochemistry assays. The present sequence represents a cDNA clone Sequence 9796 BP; 2064 A; 2679 C; 2566 G; 2487 T; 0 U; 0 Other; Claim 1; SEQ ID NO 616; 1323pp; English hypersensitivity disorders. Rosen CA, Ruben SM; WPI; 2003-140218/13. from ATCC deposit. WO200290526-A2. Homo sapiens 14-NOV-2002 15-JAN-2004 ADD38134; RESULT 15 

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Similarity

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Query Match Best Local 9

1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG 60

New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, or related immediate human secreted protein; Antiallergic; Antiinflammatory; Antibacterial; Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss. 5988 AAAATCCAGCCTGAGTCTCACCAGG 6013 BP cDNA clone in ATCC deposit #28. ADD38134 standard; cDNA; 9796 21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P. 19-MAR-2002; 2002WO-US008279 (HUMA-) HUMAN GENOME SCI INC. (first entry) 셤

180 AAAAATCCAGCCTGAGTCTCACCAGG 6013 181 AAAAATGCAGACTGTGATTCAGCAGG 206 4, 2005, 08:31:24 completed: August ne : 203.826 secs 5928 5988 셤 ð g ઠે

CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120

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AW502237 UI-HF-BR0 AQ44879 CITBI-E1-B67141 CIT-HSP-201 AQ045355 CIT-HSP-2 AA834707 od99d03.s BX411272 DKCZp686H AQ047216 RPCIII-42 BQ775109 UI-H-FH0-AV711465 AV711465 BZ612108 WHACNOZTF BF913236 IL3-UT011

AQ348991 RPCIII-12 AQ470077 CITBI-EL-AAG1938 aC59802.8 AA011026 ze34C08.8 B69029 CIT-HSP-202 AQI12051 CIT-HSP-2 BF337320 CIT-HSP-2 AG144102 Pan trog1

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1149 row: E column: 4
Seq priner: T7
Class: BAC ends
High quality sequence stop: 828.
Location/Qualifiers
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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genomic clone Plate=1149 Col=4 Row=E, genomic survey sequence.
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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|mol_trype="genomic DNA"
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AQ5750780 HS 5576 B

AQ313572 RPCI11-ID

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AQ474644 CHTB1-E1-

AQ490406 RPCI-11-21

CF128315 UI-HF-ETO

AW410354 RPCI11-10

AG047289 Pan trogl

AG12235 RPCI11-10

AG14229 Pan trogl

AG16213 Pan trogl

AG160213 Pan trogl

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 (bases 1 to 34)

Nagas (b. Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Gagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.W., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
futp://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-ET0121-
311000-658-f04&t3=2000-10-31&t4=1)
Seq primer: puc 18 forward
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CMO-ET0121-311000-658-£04 ET0121 Homo sapiens cDNA, mRNA sequence.
BF871137
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                   1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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                                                                                                                                                                                                                                                                                CTGAGGCAGGAGCACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                       Length 828;
                                                                                                                                                              Indels
                                                                                                                       Query Match 51.6%; Score 154.8; DB 8; Best Local Similarity 73.1%; Pred. No. 8.9e-20; Matches 198; Conservative 0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AATGGCACTTAACTACTTGGAGGTCATGGAT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 crececrecarecaecrecececerecar 244
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/organism="Homo sapiens"
/mol_type="mRNA"
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High quality sequence stop: 331.
Location/Qualifiers
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BF871137
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
Ingolstaedter Landstr.1, D-85764 Neuherberg, German
This is the 5' sequence of the clone insert Clone from S. Wiemann,
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; sequenced by BMF2 [Biomedical
Research Center at the Hahridh-Heine-University,
Duesseldorf/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKF2P459P1831) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GBRMANY; Email:
clonedrzpd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdma/.
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone lib="BT0121"
/note="Organ: lung_tumor; Vector: puc18; Site 1: Smal;
/note="Organ: lung_tumor; Vector: puc18; Site 1: Smal;
/note="Organ: lung_tumor; Vector: puc18; Site 1: Smal;
/note="Organ: lung_tumor; Vector: puc18; Site 1: Smal;
/note="Organ: lung_tumor; Vector: pactor application
/no. 196,716 - Ludwig Institute for Cancer Research)
/no. 196,716 - Ludwig Institute for Cancer Research
/notiles into the puc 18 vector. Reverse transcription of
fissue mRNA and cDNA amplification were performed under
low stringency conditions."
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pcorl) Pongo pygmaeus cDNA clone
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(bases 1 to 526)
Koehrer,K. Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
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0
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Pred. No. 5.6e-19;
0; Mismatches 35; Indels
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/mol type="mRAM"
/db xref="taxon:9600"
/clone="DKPZp459P1831"
/tissue type="cortex"
/dev stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATGCAGACTGTGATTCAGCAGGT 207
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DKFZp459P1831_5', mRNA sequence.
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Pongo pygmaeus
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organism="Homo sapiens"
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/db_xref="GDB:7538536"
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                                                                                                 Query Match
Best Local Similarity 87.3%;
Matches 165; Conservative
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Homo sapiens
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AQ313572/c
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htc.washington.edu
Plate: 1152 row: J column: 8
Seq primer: T7
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ750780 800 bp DNA linear GSS 19-JUL-1999 HS_5576_B2_E04_T7A_RPCI-11 Human Male BAC_Library Homo sapiens genomic clone Plate=1152_Col=8 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
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                                                                                                                                                                                                                                CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
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                                                                                                                                                                                                                                                                                                           387 AAAATACAAAATTAGCCAGGCATGGTGGCACGTGCCTGTAATCCCAGCTACTCAGGAGG 328
                                                                                                                                                         9
/clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                       1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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                                                                                                                   Gaps
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                                                                            Length 526;
                                                                                                                 Indels
                                                                                                                   20;
                                                                        Score 151; DB 7;
Pred. No. 5.2e-19;
0; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1152 Col=8 Row=J"
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Location/Qualifiers
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                                                                          Query Match
Best Local Similarity 89.1%;
Matches 163; Conservative
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Homo sapiens
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AQ750780
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.

E I (bases 1 to 675)

S Adame, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Orber GSSs: RPCII-101F7. TJ

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
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Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library and albability, please conteact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seg primer: T7

Class: BAC ends.
and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAGGCAGGAGCACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
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tes 24;
                                                                                                                                                               Score 150.6; DB 8;
Pred. No. 5.7e-19;
0; Mismatches 24;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                    385 AAAGAGCCAGACAGTAAATC 404
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                     61
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AQ474644/c
LOCUS
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                                                                                                                                  /clone lib="Human MCF7 breast cancer cell line library (MCF7_1)"
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                                                   Indels
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This clone is available from Amplicon Express
http://www.genomex.com
     DB 8;
                                6.4e-19;
Query Match
So.1%; Score 150.4; I
Best Local Similarity 88.6%; Pred. No. 6.4e-
Matches 163; Conservative 0; Mismatches
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Homo sapiens
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Colin Collins' lab
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Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: hbe@rigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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1 (bases 1 to 565)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Wenter,J.C.
Wen be of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                         S65 bp DNA linear GSS 23-APR-1999 CITB1-E1-2584M11.TR CITBI-E1 Homo saplens genomic clone 2584M11, genomic survey sequence.
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/db_xref="taxon:9606"
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University of Iowa

375 Mewton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 9260

Rax: 319 335 9265

Rax: 319 335 9265

Email: bento-coarec@ulowa.edu

Tissue Procurement: Mary Hendrix

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/humanfl.html

The following repetitive elements were found in this CDNA

sequence: 579-751, >ALU (matched compliment)

Seq primer: pyx.5.
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is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-HF-ETO-awf-o-16-0-UI.ț1 NIH MGC_214 Homo sapiens cDNA clone
MRASE:30555903 5', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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Other GSSe: RPGI-11-244E4 TJ

Other GSSe: RPGI-11-244E4 TJ

Other GSSe: RPGI-11-244E4 TJ

Other GSSe: RPGI-11-244E4 TJ

Other GSSe: RPGI-11-244E4 TJ

Other Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Email: hbe@tipr.org
Email: hbe@tipr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from Research Genet cs (info@resegen.com). BAC end search page:
Rttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                              RPCI-11-244E4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-244E4, AQ490406
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (Dases 1 to 657)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
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BAC End Sequences from Library RPCI-11 for Sequence-Ready
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//note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
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GSS.
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181 AAAAATG 187
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Best Local Simi
Matches 188;
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/organism="Homo sapiens"
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GSS.
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Best Local Similarity
Matches 170; Conserv
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181 AAAAA 185
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="INAGE:2961538"
/lab hoft="HOMO sarcoma"
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/clone lib="NIH_MGC_17"
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/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: GCORI; Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following S; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1990)

Unpublished (1990)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lnage.image.html

Plate: LLCMSG row: K column: 11

Seq primer: M13RP1 reverse primer (ABI).
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                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 8.9e-19;
0; Mismatches 22; Indels 0
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Best Local Similarity 88.1%;
Matches 163; Conservative
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                                                                                                                                      567 AAAGTCCAGA 557
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RPCI11-73B12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-73B12,
genomic survey sequence.
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1 (bases 1 to 572)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdddams@rigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
Reparch Genetics (info@resgen.com). BAC end search page:
Seq primer: SP6
Class: BAC ends.
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/note="Vector: pBACe3 6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 49.9%; Score 149.6; DB 8; al Similarity 83.3%; Pred. No. 9.4e-19; 170; Conservative 0; Mismatches 34;
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2 (Dases I to 94.7).

Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (U2.AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIERN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(R-mall:chimpbe@69sc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
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Pan troglodytes DNA, clone: RP43-025P15.T7, genomic survey
sequence.
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Ban troglodytes
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="pen troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="pTB-026M07.F"
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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AG160213.1 GI:16689891
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RPCII1-103E16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-103E16,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/clone lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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83.3%; Pred. No. 9.2e-19;
iive 0; Mismatches 34;
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mol_type="genomic DNA"
db_xref="GD8.7539279"
/db_xref="taxon:9606"
/clone="RPCI-11-103E16"
/sex="Male"
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GSS.
                                                                                                                                                                                    Homo sapiens (human)
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Matches 170; Conservative
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A0312235
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1 (Dases I to 72)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 10-NOV-1999
                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.

Direct Submission
Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
TT=1:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCT-43 This BAC
end was generated during the R&D process and may have higher chance
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sapiens genomic clone Plate=3100 Col=21 Row=1, genomic survey
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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84.4%; Pred. No. 9.9e-19;
ive 0; Mismatches 31;
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Best Local Similarity 84.4
Matches 168; Conservative
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High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
BAC end web Server: http://www.htsc.washington.edu
BAC end web Server: http://www.htsc.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end web Server: http://www.htsc.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
Clones may be purchased from Research Genetics (info@resgen.com).
Clones may be purchased from Research Genetics (info@resgen.com).
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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Matches 177; Conservative 0; Mismatches 46; Indels 0
Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Location/Qualifiers
1.732
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177920,
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-104046
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Maximum Match 100%
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RESULT 2 2.09-949-016-14253 ; Sequence 14253, Application US/09949016 ; Patent No. 6812339 ö

Gaps

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Indels

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Matches 178; Conservative
    Matches 179; Conservative
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| Sequence 12366, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| THERE OF INVENTER, J. Craig et al. | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF | FILE REFERENCE: CLOOU1307 | CURRENT APPLICATION NUMBER: US/09/949,016 | CURRENT FILING DATE: 2000-04-14 | PRIOR FILING DATE: 2000-10-20 | PRIOR FILING DATE: 2000-10-20 | PRIOR FILING DATE: 2000-10-03 | PRIOR APPLICATION NUMBER: 60/231,768 | PRIOR APPLICATION NUMBER: 60/231,498 | PRIOR APPLICATION NUMBER: 60/231,498 | PRIOR APPLICATION NUMBER: 60/231,498 | PRIOR APPLICATION NUMBER: 60/231,498 | PRIOR APPLICATION NUMBER: 60/231,498 | PRIOR APPLICATION NUMBER: 2000-09-08 | NUMBER OF SEQ ID NOS: 207012 | SEQ ID NO 12366 | LENGTH: 23155 | LENGTH: 23155
                            JAPELICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERBUCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELLING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 14253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24497;
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Pred. No. 2.1e-38;
0; Mismatches 31;
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LCCATION: (1)...(23155)
COTHER INFORMATION: n = A,T,C or G
US-09-949-016-12366
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81.4%;
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85.0%;
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Matches 175; Conservative
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US-09-949-016-12366
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US-09-949-016-14253
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Best Local Similarity

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RESULT 4

US-09-949-016-80246/c

US-09-949-016-80246, Application US/09949016

Setent No. 681233

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: US/09/949,016

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

LENGTH: 601
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; Sequence 14046, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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RESULT 7
US-09-949-016-12216/c
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US-09-949-016-12216
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LENGTH: 36759
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Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESERVE FREESEQ FOR WINDOWS VERBION 4.0
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-hes 40; Indels
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           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-16
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
SPRIOR PILING DATE: 2000-10-03
SOFTWARE: PASCE OF WINDER: 6/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASCE OF WINDOWS VERSION 4.0
SEQ ID NO 14046
                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1)...(68173)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 84.7%;
Matches 172; Conservative (
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Matches 178; Conservative
FILE REFERENCE: CL001307
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US-09-949-016-78059
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LENGTH: 601
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1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG

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Sequence 12216, Application US/09949016

Patent No. 6812339

Patent No. 681239

TITLE OF INVENTION: POLYWORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/2414

PRIOR APPLICATION NUMBER: 60/241, 758

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231, 768

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR FILING DATE: 2000-00-03

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06

PRIOR FILING DATE: 2000-00-06
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                                                                                        14576 AAAATAGAAAAATTAGCCGGGCATGGTGGCACCTGTAGTCCCAGCTACTTGGGAGG
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; Sequence 12577, Application US/09949016
; Patent No. 6812339
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US-09-949-016-12577
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Sequence 204867, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL1307

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-06-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRANKE: FRANKES

SOFTWARE: FRANKE: FRANKES

SOFTWARE: FRANKES

LENGTH: 601

LENGTH: 601
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Pred. No. 2.3e-37;
0; Mismatches 31;
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Pred. No. 4e-38;
0; Mismatches
           PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 36760
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Best Local Similarity 89.2%;
Matches 165; Conservative
                                                                                                                                                                                                                     51.1%;
ilarity 84.7%;
Conservative (
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Matches 172; Conserv
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US-09-949-016-204885/c
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                                                                                                                                                                            ORGANISM: Human
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Sequence 17299, Application US/09949016

Sequence 17299, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICATI: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17299
FACENTEAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NOS: 2577
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Best Local Similarity 81.8%; Pred. No. 2.7e-37;
Matches 189; Conservative 0; Mismatches 40
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Pred. No. 5.6e-37;
0; Mismatches 20; Indels 0;
                                                                                                                                                                         Score 153; DB 4; Length 30222;
Pred. No. 2.7e-37;
0; Mismatches 40; Indels 2
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US-09-949-016-17533/c
Sequence 17533, Application US/09949016
; Petent No. 6812339
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Best Local Similarity 89.2%;
Matches 165; Conservative
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Best Local Similarity 81.8 Matches 189; Conservative
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                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17299
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LENGTH: 30222
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Sequence 204886, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FasteEQ for Windows Version 4.0
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Batent No. 6812339
GENERAL INCORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-0-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEEQ for Windows Version 4.0
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Pred. No. 5.4e-38;
1; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 152.6; DB 4
Pred. No. 5.4e-38;
1; Mismatches 20
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Best Local Similarity 88.6
Matches 164; Conservative
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Best Local Similarity 88.6
Matches 164; Conservative
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US-09-949-016-204887/c
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RESULT 15

US-09-949-016-143301

Sequence 143301, Application US/09949016

Sequence 143301, Application US/09949016

Recent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTHARE FREE FREE SEQ for Windows Version 4.0

SEQ ID NO 143301

TYPE: DNA

TYPE: DNA

CREANISM: Human

US-09-949-016-143301
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                                                                                          266 CTGAGGCATGAGAATCACTTGAACCCAGGAGGGGGAGGTTGCAGTGAGCCGAGATCGAGC 207
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1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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Job time : 64.8219 secs
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| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7297361 seqs, 3241162794 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli						S
SUMMARIES	D CI	00 9 US-09-899-276-6	US-10-685-705-4	US-10-311-455-1625	US-10-322-281-712	US-10-027-632-128663	US-10-027-632-128663	US-09-764-847-1214
	DB	6	19	15	19	13	11	0
	Length	300	11793	5926	31926	552	552	5304
	% Query re Match Length DB ID	300 100.0 300 9 U	100.0	55.9	53.6	52.2	52.2	52.1
	Score	300	300	167.8	160.8	156.6	156.6	156.4
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## **ALIGNMENTS**

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APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Coy, Johannes
APPLICANT: Coy, Johannes
APPLICANT: Poustka, Annemarie
APPLICANT: Poustka, Annemarie
APPLICANT: Parzelt, Andrea
APPLICANT: Parzelt, Andrea
TITLE OF INVENTION: No. US20020106355A1e1 Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: No. US20020106355A1e1 Regulatory Sequences
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ 1D NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 300;
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100.0%; Pred. No. 8.4e-82;
ative 0; Mismatches 0;
                      Sequence 6, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 300; Conservative
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; ORGANISM: Homo sapiens
US-09-899-276-6
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LENGTH: 300
US-09-899-276-6
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Sequence 4, Application US/10685705

Publication No. US20040177387A1

GENERAL INFORMATION:

APPLICANT: University of Kentucky Research Foundation

APPLICANT: University of Kentucky Research Foundation

TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular

TITLE OF INVENTION: Degeneration

TITLE OF INVENTION: USGENER: US/10/685,705

CURRENT APPLICATION NUMBER: US/10/685,705

CURRENT FILING DATE: 2003-10-16

PRIOR FILING DATE: 2002-10-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 10
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1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                        1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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; Pred. No. 4.1e-81;
0; Mismatches 0;
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US-10-311-455-1625
; Sequence 1625, Application US/10311455
; Publication No. US20030143606A1
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Best Local Similarity 100.0%;
Matches 300; Conservative 0
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US-10-685-705-4
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APPLICANT: DIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kur.
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
FILE REPERBROE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 112, Application US/10322281

Sequence 112, Application US/10322281

Publication No. US20040126762A1

GENERAL INFORMATION:
APPLICANT: David W. Morris

TITLE OF INVENITION: Novel Compositions and Methods in Cancer
TITLE OF INVENITION: Novel Compositions and Methods in Cancer

TITLE OF INVENITION: Novel Compositions and Methods in Cancer

TURRENT APPLICATION UNGBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
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Pred. No. 1.3e-40;
0; Mismatches 47
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Best Local Similarity 80.7%;
Matches 196; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.8
Matches 177; Conservative
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378 AAAATACAAAAATTAGCCAGGCATGGTGGCATGTGCCTGTAGTCCCAGCTACTCGGGAGG 319
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Lidentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PAPLICATION NUMBER: US 60/210,006
PRIOR PLICATION NUMBER: US 60/190,676
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-24
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Patent No. US20020132767A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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Pred. No. 1.2e-37;
0; Mismatches 19; Indels
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Pred. No. 3.8e-37;
0; Mismatches 41;
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Best Local Similarity 89.8%;
Matches 168; Conservative (
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81.5%;
       Publication No. US20030204075A9
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Best Local Similarity 81.5
Matches 181; Conservative
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US-09-764-847-1214/c
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US-10-027-632-128663
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LENGTH: 5304
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR PELING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 128663, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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US-10-027-632-128663/c
; Sequence 128663, Application US/10027632
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US-10-027-632-128663/c
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| Sequence 1125, Application US/09764847 |
| Patent No. US20020132767A1 |
| SEMERAL INFORMATION: |
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies |
| TITLE OF INVENTION: NUMBER: US/09/764,847 |
| CURRENT FILING DATE: 2001-01-17 |
| Prior application data removed - consult PALM or file wrapper |
| SEQ ID NOS: 2003 |
| SEQ ID NO 1215 |
| LINGTH'S 3044 |
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/ Sequence 1214, Application US/10092154
/ Publication No. US20030054375A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TILLE OF INVENTION:
/ TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ TILLE REFERENCE: PC009C1
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 2003
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 1214
/ LENGTH: 5304
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Pred. No. 3.8e-37;
0; Mismatches 41;
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Best Local Similarity 81.5%;
Matches 181; Conservative 0
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CORGANISM: Homo sapiens
US-09-764-847-1215
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US-10-092-154-1214/c
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Publication No. US20020198371A1;
GENERAL INFORMATION:
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Pred. No. 3.8e-37;
0; Mismatches 41; Indels 0;
                                                      DB 14; Length 5304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1215, Application US/10092154
; Sequence 1215, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT PELING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; SEQ ID NO 1215
; LENGTH 5304
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                                                      Query Match 52.1%; Score 156.4; DB 14; Best Local Similarity 81.5%; Pred. No. 3.8e-37; Matches 181; Conservative 0; Mismatches 41;
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Best Local Similarity 81.5%;
Matches 181; Conservative C
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US-10-092-154-1215
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 3426, Application US/10723860

Publication No. US20040253606A1

Publication No. US20040253606A1

REWIRAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: MUMBER: US/10/72,860
CURRENT APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739

NUMBER OF SEQ ID NOS: 8939

SOFTWARE: Patentin version 3.2
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                                                                                                                                         Score 155.8; DB 17; Length 556;
Pred. No. 2.2e-37;
0; Mismatches 17; Indels 0;
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                                                                                                                                            51.9%;
                                                                                                                                       Query Match
Best Local Similarity 90.7'
Matches 166; Conservative
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ORGANISM: Homo sapiens
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US-10-027-632-128664/c
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US-10-723-860-3426/c
                                                                                            US-10-027-632-128662
                                             TYPE: DNA
ORGANISM: Human
SEQ ID NO 128662
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Pred. No. 2.2e-37;
0; Mismatches 17;
            CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PAILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
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PRIOR PILING DATE: 1999-09-09
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CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2002-04-30
PRIOR PLLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 3090-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-12-36
PRIOR FILING DATE: 1999-12-36
PRIOR FILING DATE: 1999-12-36
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PRIOR FILING DATE: 1999-08-09
SEQ ID NOS: 325720
SOFTWARE: FastesEQ for Windows Version 4.0
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 166; Conservative
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LENGTH: 556
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Search completed: August 4, 2005, 15:54:26 Job time : 539.142 secs
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Best Local Similarity 90.2%;
Matches 165; Conservative
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                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-128664
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Sequence 128664, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANTY WANG, David G.
TITLE OF INVENTION: IOBACIA:
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PLICATION NUMBER: US 60/198,676

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23
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                                     1 AAAATATAAAAATTAAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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51.8%; Score 155.4; DB 13; Length
Best Local Similarity 90.2%; Pred. No. 2.9e-37;
Matches 165; Conservative 1; Mismatches 17; Indels
Sequence 128664, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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61 CTGAGGCAGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
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                                                                                                                                                                                                                Score 155.4; DB 17;
pred. No. 2.9e-37;
1; Mismatches 17;
PRIOR APPLICATION NUMBER: 05. 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 05. 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for LENGTH: 556
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ACL18439 Rattus no
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ACL101018 Rattus no
ACL15173 Rattus no
AF769026 Unculture
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ACL12913 Rattus no
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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    .650
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 7 from Patent EP1170372.
AX343334
         AC114440
MMU238892
AC022299
                                         AF079313
AK655393
AC166739
AC118439
AC118439
AC113158
AC115173
AC115173
AF269026
AC106086
BX936393
AC102101
AC112101
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AP000251
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Homo sapiens
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227406
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AC005549 Homo Sapi
AX357296 Homo Sapi
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AX34659 Sequence
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AX34559 Sequence
AX43559 Homo Sapi
AF493697 Homo Sapi
AF493699 Papio ham
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AL626807 Mouse DNA
AL713839 Mus muscu
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                                                                     August 3, 2005, 21:53:02 ; Search time 2612.63 Seconds (without alignments) 12055.236 Million cell updates/sec
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Homo sapien
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                                                                                                                                   ggcttgtgccgagatgttcc.....aattgaatgcggtccaccaa 650
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
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Maximum DB seq length: 200000000
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dicine ractant prote AATFIPQGLAQP"	100.04;   Score 650;   De 9;   Length 327;
181 AGCGGGGGGGGCATTTTTTTTTTTTTTTTTTTTTTTTTT	HUMMORPH HUMMORPH 13227 bp DNA linear PRI 14-APR-2000 DEFINITION Unan gene for monocyte chemoattractant protein-1, 5'-genome region.  ACCESSION D26087.1 GI:516772 HOMO sapiens (human) D26087.1 GI:516772 HOMO sapiens (human) D26087.1 GI:516772 HOMO sapiens (human) D26087.2 GI:516772 HOMO sapiens (human) D26087.2 GI:516772 HOMO sapiens (human) D26087.3 MCP-1; monocyte chemoattractant protein-1. MWENTORY BURNAYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammila; Butheria; Primates; Catarrhini; Hominidae; Homo. MWENTOR: Rolling, B.J., Stier, P., Einse, T. and Wong, G.G. TITLE MEDINE D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D1007880 D100

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9174 bp DNA linear PRI 09-JUL-2002 Homo sapiens small inducible cytokine A2 (monocyte chemotactic AF519531 AF519531.1 GI:21435976
                                                                                                                                                                                                                                                                       4797 GECTTGTGCCGAGATGTTCCCAGCACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCA 4856
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I (basel 1 to 9174)

Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A., Rajkumar,N., Toth,E.J., Yi,Q. and Nickerson,D.A.

Bujrect Submission
Submitsed (06-JUN-2002) Genome Sciences, University of Washington, 1705 ME Pacific, Seattle, WA 98195, USA
To cite this work please use: SeattleSNPs. NHLBI HL66682 Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4857 GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCA
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                                                                                                                           Query Match 94.9%; Score 616.6; DB 9; Best Local Similarity 97.7%; Pred. No. 1.2e-179; Matches 636; Conservative 0; Mismatches 14;
     8968. .>9073
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for Genomi http://pge FEATURES BOUTCE	10.1104		variation	variation	variation	variation	variation	gion		variation	variation	variation	variation	variation	variation	variation	variation	repeat_region	variation	variation	variation	variation	variation

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Submitted (127-AUG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Shases 1 to 1474[6]

Birran, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Porrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagoes, B., Heaford, A., Herena, L., Horton, L., Howland, J. C., Jones, C., Kann, L., Kartas, A., Lehoczky, J., C., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, R., Marfquis, N., McBwan, P., McGurk, A., McKernan, R., Marff, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stolanovic, N., Stone, C., Stange-Thomann, N., Stilwell, J., Wheeler, J., Wu, Y., Wyman, D., Ve, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Ve, W.J., Zhao, J. and Zody, M., Stone, C., Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                  ACO05549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
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1. (bases 1 to 147416)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chronosome 17, clone hRPK.215_E_13

Unpublished
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                                     480 CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419
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Pred. No. 3.9e-179;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /frequency="0.01"
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                                                                                                                                                                                                                                                                                                                                    /frequency="0.03"
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                                                                                           /replace="t"
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3072
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Score 615; DB 9; Length 147416;
Pred. No. 4.5e-179;
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/rpt_family="purine-rich"
complement (42486. 42569)
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/rpt family="MIR"
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complement(16483. .16653)
/rpt_family="MIR"
16830. .16949
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ement (ATC)
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complement (48165. .48209)
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9362. .39414
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complement (27814. .27950)
rpt family="MER94"
                                                                        /rpt_family="MER9"
complement(12983. .13257)
/rpt_family="AluJb"
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/rpt family="AT rich"
:complement(40152. .404
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/rpt_family="LTR16A"
17393. .18306
/rpt_family="HBRVL"
18315. .24307
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rpt family="AT_rich"
9960. .30341
                                                                                                                                                                                                                                                                                                               rpt_family="LiPA2"
4309. .24335
rpt_family="AT_rich"
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24513. .25245
/rpt_family="HERVL"
25613. .25758
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44781. .44811
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2364. .32581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="Alusx"
complement(33593. ..
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11567. .11836
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                                                                                                                           5248. .15364
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1297<u>9</u>.
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       Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Porrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagoes, B., Haeford, A., Herena, L., Horton, L., Howland, J. C., Jones, C., Kami, L., Horton, L., Howland, J. C., Jaccott, L., Jones, C., Kami, L., Horton, L., Mckernan, K., Mcdonald, P., Marquis, N., McEwan, P., McGurk, J., McKernan, K., Malla, M., Morris, W., Morrow, J., Mychalecky, J., Nahla, M., Morris, W., Morrow, J., Mychalecky, J., Nahla, M., Morris, W., Morrow, J., Mychalecky, J., Studner, D., Roy, A., Severy, P., Stunger-Thoman, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Toruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.

Li Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA Research, 320 Charles Street, Cambridge, Ma 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, M. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                     Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project L228). The first 2Kb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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clone_lib="RPCI-11 human BAC library"
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/rpt_family="MIR"
10109. . 10258
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complement (5430. .5549)
/rpt family="FLAM"
complement (5941. .6051)
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/db_xref="taxon:9606"
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980. .3131
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/db_xref="taxon:9606" 2255321 /gene="MCP1" /note="HSMCR30; MCP-1" promoter 2252746 /gene="MCP1" variation 225	/replace="c" variation 668 /gene="WCP1" /note="SNP" /replace="t"		TATA_signal 7.2714	1 1-	/protein id="AAQ75526.1" /db_xref="G1:34559720" /translation="MKVSAALLCLLIIAATFIPQGLAQP"	Origin  Query Match  Best Local Similarity 97.7%; Pred. No. 3.5e-177;  Matches 628: Conservative 0: Mismarches 14: Indels 1: Gans 1:	9 CCGAGATGTTCCCAGCACACCCCATGTGAGAGCTCCCTGGCTCCGGGCCCAGTATCTGG 68	69 PATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCAAAGCTGCC	Db 181 AGGGCATCTTTCTTGACAGAGCAGAAGTGGGGAGGCAGACTGTCACTTTCCAGAAGA 240  Qy 249 CTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAG 308  Db 241 CTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAG 300	OY 309 GCCAAGTCACTTTCCAGAGATGACTCCTTCCTGAAGTAGAGACATGCTTCCAACACT 368	Oy 369 CAGAAGCCTAIGIGAACACTCAGCCAGCAAAGCT-GGAAGITTTTCTCTGTGACCAICGG 427 	Qy 428 CTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCAC 487
Matches         635;         Conservative         0;         Mismatches         15;         Indels         1;         Gaps         1;           Qy         1	121 AAGCTGCCTCCTCAGAGTGGGAATTTCCACTCACTCTCTCACGCCAGCACTGACCTCCC	64050 AGCGGGGGGCATCTTTTCTTGACAGAGGGGAGAAGTGGGAGGCAGACAGCTATCACTTT  241 CCAGAAGACTTTCTTTTCTGATTCATACCCTTCCCTGTGTTTACTGTCTGATAT  63990 CCAGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATAT  63990 CCAGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTTTACTGTCTGATAT	Qy         301 ATGCAAAGGCCAAGTCACTTTCCAGAGATGACAACTCCTGAAGTAGAGACATGCTT 360           Db         63930 ATGCAAAGGCCAAGTCATTCCAGAGATGACAACTCCTTCCT	ACCATGGGCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGT 	OY 480 CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG 539  [	Oy 540 ACTAAGCCAGGAGACTTATTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGA 599  [	OY 600 AAACCCGAAGCATGATTATAAAGGGAATTGAATGCGGTCCACCAA 650 	RESULT 6 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY357296 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY35729 AY	Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 3221)  AUTHORS Nyquist, P.A. and Degraba, T.J.  TITLE Two New Single Nucleotide Polymorphisms (SNPs) in the MCP-1  Promoter in Patients with Carotid Atherosclerosis: Transcriptional Induction and New Protein Binding Stee	JOURNAL IMPORTANCE OF TOTAL BILLING SILES REFERENCE 2 (bases 1 to 3221) AUTHORS Nyquist, P.A. and Degraba, T.J. TITLE Direct Submission	AL Submitted Falls Chur S	Source 13221 /organism="Homo sapiens" /mol_type="genomic DNA"

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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Submitseion and Landers of Stokenson washington equi/RW/RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens chromosome 17 clone RP11-329H16 map 17, LOW-PASS
SOCIENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP11-329H16

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                 421 CTAATTGGTCTCCTTCTGGATTGTGGCTTTATCAGATAAAAACAAGTGGTCATGCCAC 480
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                                                                        <u> AGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCC</u>
                                                                                                        548 AGGAGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCCGA
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Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 15499
Center clone name: 329_H_16
                                                                                                                                                                                                                                                                                                                                   AGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
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Homo sapiens (human)
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DB 2; Length 73806;

Score 425.2;

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xrefe="texorn:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1626 03-JAN-2002;
Epigenomics AG (DE)
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  Pred. No. 3.4e-120;
0; Mismatches 63;
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Sequence 1626 from Patent WO0200928.
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Matches 496; Conservative
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AF493701 316 bp DNA linear PRI 12-MAY-2002 Callithrix jacchus monocyte chemoattractant protein 1 (MCP1) gene,
                                                                                                                      II, National Institute of
J.N.U. Campus, New Delhi 110 067,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             callithrix jacchus (white-tufted-ear marmoset)
Callithrix jacchus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae;
Callithrix.
                                                                                                                                                                                                                                                                                      480 CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG
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  grancrggaargcaggcrccaargcarrcrcrrcracgggarcrggaagcrrcca
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Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K.
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/ pote="monocyte chemoattractant protein
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/db_xref="taxon:9483"
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Submitted (21-MAR-2002) Virology
Immunology, Aruna Asag Ali Marg,
India
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3684 CTTATACCGAAATATTCCCAACACACACCCCATATAAAAACTCCCTAACTCCGAACCCAAT 3625
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/organism="synthetic construct"
/mol.type="unasigned DNA"
/db xref="texon:32630"
/nofe="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGCTTGTGCCCGAGATGTTCCCAGCACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGAC
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                                      GCTGCCTCCAGAGTGGGAATTTCCACTCACTCTCTCACGCCAGCACTGACCTCCCAG
                                                                                           243 AGAAGACTITICTITICTGATICATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATAT
                                                                                                                                                                                                                                   CATGGGCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAACAAGTGAGTCA
                        ATCTGGAATGCAGGCTCCAGCCAAATGCATTCTTCTACGGGATCTGGGAACTTCCAAA
                                                                                                                                CGGGGGGAGGGCATCTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 1625 03-JAN-2002; Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 365.4; DB 6;
Pred. No. 1.1e-101;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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synthetic construct
other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1625 from Patent WO0200928.
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llarity 73.6%;
Conservative
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Matches 479; Conserv
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AX346554
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AF493700 312 bp DNA linear PRI 12-MAY-2002
Macaca radiata monocyte chemoattractant protein 1 (MCP1) gene,
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Homo sapiens isolate 1 monocyte chemoattractant protein 1 (MCP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505
                                                                                                                                                                                                                                                                                         Banerjea,A.C.
Direct Submission
Submitted (21-MAR-2002) Virology II, National Institute of
Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 GATTGTGGCTTTGCTCAGATAAAAAGAAGTG-GCCATGCGACAGGATGTCTGTAAGCCCA 287
                                                                                                                                                   Macaca radiata (bonnet macaque)
Macaca radiata
Macaca radiata
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 312)
Shanmugasundaram,G.K., Chakraborti,S., Sankaranarayanan,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banerjea,A.C.
Direct Submission
Submitted (21-MAR-2002) Virology II, National Institute of
Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067,
India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bumanlia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 310)
Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTATGTGAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTGTGGCTT--ATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCA
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21.4%; Score 139; DB 9; Length 312;
Best Local Similarity 86.3%; Pred. No. 1.6e-31;
Matches 177; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MCP1"
/note="monocyte chemoattractant protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                           1. .312
/organism="Macaca radiata"
/mol_type="genomic DNA"
/db_xref="taxon:9548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGATTCTGGGATTCTATGAGTGAT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TTGACTCTGGAATTCTATGAGTGAT 312
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                 AF493700.1 GI:20530676
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AF493697
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/gene="MCP1"
                                                                               promoter region.
AF493700
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KEYWORDS
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   RESULT 12
AF493700
LOCUS
                                                           DEFINITION
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JOURNAL
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AF493697
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Homo sapiens isolate 2 monocyte chemoattractant protein 1 (MCP1)
                                                                               387
                                                                                                                 171
                                                                                                                                                         445
                                                                                                                                                                                               231
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                                                                                                                                                                                                                                                     232 TGGATTGTGGCTTTATCAGATAAAAACAAGTGGTCATGCCACAGGATGTCTATAAGCCCA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 307).
Shanmugasundaram,G.K., Sankaranarayanan,K. and Banerjea,A.C.
Direct Submission
Submitted (21-MAR-2002) Virology II, National Institute of Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTATGTGAACAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 ACGCCAGCACTGACCTCCCAGCCAGACATGCTTCCAACACCCCAGAAGCCTATGTGAAACAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 TCAGCCAGCAAAGCT-GGAAGTTTTCTCTGTGACCATGGGCTAATTGGTCTCCTTCTT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 TCAGCCAGCAAAGCTGGGAAGTTTTCTCTGTGACCATGGGCTAATTGGTCTCCTTCTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATTGTGGC-TTATCAGATAAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCA 505
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                                                                                                                                                   328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTATGTGAACAC
                                                                                                                                                                                                                             TGGATTGTGGCTTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCA
                                                                                                             112 AcGCCAGCACTGACCTCCCAGCGAGACATGCTTCCAACACTCAGAAGACCTATGTGAACAC
                                         Gaps
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                                         5;
     Length 316;
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<1. ->307
/gene="MCP1"
/note="monocyte chemoattractant protein 1"
/gene="MCP1"
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                         27;
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     DB 9;
   Score 147.8; DB 9
Pred. No. 2.9e-34;
0; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .307
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                               TTGATTCTGGGATTCTATGAGTGAT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/isolate="2"
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AF493698
Query Match 22.7%;
Best Local Similarity 85.9%;
Matches 176; Conservative
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Homo sapiens
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Best Local Similarity 90.23
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                           206
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
AF493698
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JOURNAL
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184 GGGGGAGGGATCTTTCTTGACAGAGGGGAAGGGGGAGGCAGACTGCACTTTCCA 243
                                                                                                                                                         p DNA linear ROD 13-AUG-1994 chemoattractant protein-1 (mcp-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TCTGGAATGCAGGCTCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCAAAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2. (bases 2321 to 2787)
Rollins, B.J., Morrison, E.D. and Stiles, C.D.
Rollins, and expression of JE, a gene inducible by platelet-derived growth factor and whose product has cytokine-like properties proc. Natl. Acad. Sci. U.S.A. 85 (11), 3738-3742 (1988)
530
                                                                                     312
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 2788)
Alberta,J.A., Irminger,J. and Stiles,C.D.
Macrophage chemoattractant protein-1 (mcp-1) 5' flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jackses 1 to 2788)

Abberta, J.A.

Direct Submission
Submitted (20-JUL-1994) John A. Alberta, Cellular and Molecular
Biology, Dana Farber Cancer Institute and Harvard Medical School,
44 Binney St., Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 indingagicairincagairciccgcccaigagagagacigcinggcigcaggcccagca
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                                                           471 CAAGTGAGTCATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGAT
                                                                          253 AGAAGTGGCCATGCGACAGGATGTCTGTAAGCCCATTGATTCTGGAATTCGATGAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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/gene="mcp-1"
/product="macrophage chemoattractant protein-1"
                                                                                                                                                                                                                   14.5%; Score 94.4; DB 10; Length 2 clarity 62.2%; Pred. No. 1.2e-17; Conservative 0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="Balb/c 3T3 A31"
/cell_type="fibroblast"
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Papio hamadryas monocyte chemoattractant protein 1 (MCP1) gene,
promoter region.
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J.N.U. Campus, New Delhi 110 067,
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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1 (bases 1 to 312)
Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K. and
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0; Mismatches 26; Indels
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Submitted (21-MAR-2002) Virology
Immunology, Aruna Asag Ali Marg,
India
                                 sapiens"
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SUMMARIES

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

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Disclosure; SEQ ID NO 7; 30pp; English.

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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                           Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
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Pred. No. 1.1e-202;
0, Mismatches 14; Indels 1;
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Best Local Similarity 97.7°
Matches 636; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Ccl2-deficient; Ccr2-deficient; drusen: lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy; promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 major histocompatibility class I; MHC-I; MHC-II; Cytostatic; EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma; gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma; parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
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97.7%; Pred. No. 3.2e-200;
iive 0; Mismatches 14;
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                                                                                  This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated metular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological actuaristics and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 promoter region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recteagagragagaatticeaeteaeteeteaegeeaageaeteaeeteagegagg 180
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                Query Match 93.6%; Score 608.6; DB 12; Length 3221; Best Local Similarity 97.7%; Pred. No. 3.2e-200; Matches 628; Conservative 0; Mismatches 14; Indels 1;
analyzing development or regression of drusen and/or lipofuscin accumulation in eye.
                                                                                                                                                                                                                                                                                                                               Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
                                                           Disclosure; SEQ ID NO 3; 64pp; English
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The present invention describes an isolated polynucleotide (PN) comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN)s comprising two or more of the isolated (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. Acred 202 to Acred 424 represent sequences used in the exemplification of the present invention
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                                                                                       Human; detection; computer-readable storage medium; polymorphic site; signal carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGAAGACITICITITICIGAITCATACCCITCACCTICCCCGIGITTACTGTCTGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 GGCTTGTGCCGAGATGTTCCCAGCAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCA
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                                                              Human MCP1 nucleotide sequence >MCP1_pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 74; 93pp; English.
                                                                                                                                                                                                                                                                                                 07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                                                   07-AUG-2002; 2002WO-US025268.
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Matches 543; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV; anticonvulsant; ophthalmological; antirhemutic, antiarthritic; antidabetic, antipsoriatic, antiinflammatory; cancer; eye disease; arteriosclerosis, anaemia; acute myeloid leukaemia, Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Altheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
CCAACACTCCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCTGGGAAGTTTTTCTCTGTG
                                                                                                                                                                         CATGCCACAGGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGTGATATG
                                                                                                                                                                                                                                               CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG
                                                                                                                                                ACCATGGGCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1626
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01-SEP-2000; 2000DE-01043826
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Length 5926;

61.8%; Score 401.8; DB 6;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune system disease; cytosine methylation; antiasthmatic; antiartisclerotic; antianaemic; cytostatic; nootropic; antianaemic; anticonvolant; ophthalmologic; antirheumatic; anticonvolant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arterisoclarosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; encer; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                        3684 CTTATACCGAAATATTCCCAACACACCCCATATAAAAACTCCCTAACTCCGAACCCAAT
                                                                                                                                                                                                        3624 ATCTAAAATACAAACTCCAACCAAATACATTCTCTTCTACGAAATCTAAAAACTTCCAAA
                                                                                                                                                                                   123 GCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCCCAG
                                                                                                                                                                                                                                                                                 3324 AACACTCAAAAACCTATATAAACACTCAACCAACAAAAACTAAAAATTTTTCTCTATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTTGGGAACTTCCAAA
                                                                                                                                                                                                                                                            AGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATAT
                                                                                                                                                                                                                                                                                                                                                                                                         3384 ACAAAAACCAAATCACTTTCCAAAATAACAACTCCTTCCTAAAATAAAACATACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 TAAGCCAGGAGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACACTCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCT-GGAAGTTTTTCTCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGGGCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCACAGGATGTCTATAAGCCCATTGATTCTGGGGATTCTATGAGTGATGCTGATATGAC
   Gaps
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1625.
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 5926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL33652 standard;
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to to a plant to bacterial, fungal or yiral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAGCCTATGTGAACACTCAGCCAGGAAAGCTGGAAGTTTTTCTCTGTGACCATGG-G 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSAARKARCWYRGKGYYWAGWWWRRYKRWYWWWWYKRKYSKCSWYCKMSYYASCWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 GCCAAGTCACTTTCCAGAGATGACACTCCTTCCTGAAGTAGAGACATGCTTCCAACACT
                                                                                                                                                                                                                   bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involved in plant resistance or
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Hon
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Z,
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1.2%; Pred. No. 0.002;
ve 154; Mismatches 122;
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Xie ?
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Whitham S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 11.2%; Pr. 35; Conservative 154;
                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-IB001105
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bacterial, fungal or vira
illustrate the invention.
                                                                                                                                                                (first entry)
                                                                                                                                                                                              Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-175290/17.
                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                      WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression
                                                                                                                                                                                                                                                                          Oryza sativa.
                                                                                                                                                                                                                                                                                                                                    03-JAN-2003
                                                                                                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang H,
Katagiri 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533
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                           2841
                                                                                                      ADA71938
                                                                                                                                     ADA71938
                                                                                                                                                                                                                              Plant;
                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTAAGCCAGGAGAGACTTATTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCATGGGCTAATTGGTCTCCTTTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTACGGGATCTGGGAACTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2301 GTAİTTĞGAATĞTAĞĞTLITTAĞTTAAATĞTAİTİTTİTTİTÇĞĞĞALTTĞĞĞAATTİTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCTGCCTCAGAGTGGGAATTTCCACTCACTCTCACGCCAGCACTGACCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGGGGAGGCATCTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>AGCGGGGGGGGTATTTTTTTTTTTAGAGTAGAAGTGGGAGGTAGATAGTTATTTT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAACACTCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCT-GGAAGTTTTTCTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTTGTGCCGAGATGTTCCCCAGCACACCCCATGTGAGAGCTCCCTGGCTCCGGGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2241 GGTTTGTGTCGAGATGTTTTAGTATAGTTTTATGTGAGAGTTTTTTGGTTTTCGGGTTTTA
                                                                                                                                                                                  fragment of chemically modified gene, useful for diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 AAACCCGAAGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 365.4; DB 6; pred. No. 2.3e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 171;
                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.2%;
                 02-JUL-2001; 2001WO-EP007537
                                                  30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                         Nucleic acid comprising diagnosis and treatment
                                                                                                                             Piepenbrock C,
                                                                                              (EPIG-) EPIGENOMICS
                                                                                                                                                           WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 479; Conserv
                                                                01-SEP-2000;
                                                                                                                                                                                                                           methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
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ABL33000 RESULT

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Determination of whether compound is useful for prostate cancer treatment comprises measuring expression level of specific nucleic acid sequence in prostate cancer cell sample in the presence and absence of compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used to treat prostate cancer and comprises measuring the expression and absence of the compound. Determining whether a compound can be used to treat prostate cancer cell sample in the presence and absence of the compound. Determining whether a compound can be used to treat prostate cancer complises identifying the compound as useful for prostate cancer treatment when the expression level of the nucleic acid in the presence of the compound. Prostate cancer is usually tretaed by androgen withdrawal, by castration or through the use of an anti-androgenic drug. Bicalutamide (casodex) is one such anti-androgenic compound. The determination whether a selected compound, e.g. an anti-androgenic compound or testosterone, can be used to treat the prostate androgenic compound appreciate basis. The sequence presented is an expressed sequence tag (BST) which is more highly expressed in testosterone treated prostate cancer cells than the untreated cells.
399 GTGGATATTTGTAATTTTAGTTATTTTGGAAGTTTAGGTAGGAGAATCGTTTGAGTTTGG 458
                                              547 CAGGAGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTTAGAGAAAACCCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a method for determining whether a compound can
                                                                                              ACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCCAGTATCTGGAATGCAGGCTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, 88; prostate cancer; cancer; androgen; castration; anti-androgenic drug; bicalutamide; casodex; testosterone; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 1497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1497 BP; 397 A; 284 C; 247 G; 387 T; 0 U; 182 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36.6; DB 10;
Pred. No. 0.34;
90; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testosterone regulated prostate cancer gene #49.
                                                                                                                                               607 AAGCATGACTGGATTATAAAGGGAAATTGAA 637
                                                                                                                                                                                             519 GAGATTTTTTTAAAAATAAAAAAAAAAAAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Col 253-256; 194pp;
                                                                                                                                                                                                                                                                                                                      ADB31378 standard; cDNA; 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00220132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-595981/56.
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es 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6506607-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                       ADB31378;
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                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxeemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                   YRYSMKNYTWCTMWGYWWYWRTYMKNRYMWYKCTKTYMYWSATYWTGTWAAWMAKTKM 832
                       AGGAGAGACTIATTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCCGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAATTGGTCTCCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiartic; antidiabetic; antisoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.2; DB 6; Length 6557;
Pred. No. 0.23;
0; Mismatches 108; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 973; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 973.
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 48.8%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                     619
                                                                                                                                                                 833 RMGMTGAKTRGR 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
                                                                                                                   608 AGCATGACTGGA
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487 CAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGC 546

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/note= "Variable nucleotide A,G" 8061 /*tag= k /standard name= "Single nucleotide polymorphism" /note= "Variable nucleotide G,T" /note= "Variable nucleotide G,T" /note= "Variable nucleotide A,G" 12618 /*tag= m /standard_name= "Single nucleotide polymorphism" /standard_name= "Single nucleotide A,G" /note= "Variable nucleotide A,G"		ard name= "Single nucleotide "Variable nucleotide C,T" ard name= "Single nucleotide "Variable nucleotide A,G" s ard name= "Single nucleotide "Variable nucleotide C,G"	d d d	/Brandard_name= Singte nacted G.A" 29877 / tag= "Variable nucleotide G.A" 29877 / tag= "Single nucleotide polymorphism" / note= "Variable nucleotide deletion,CT" 30580 / tag= "Yariable nucleotide deletion,CT" / note= "Variable nucleotide G.T" 31500 / tag= "Yariable nucleotide G.T" / note= "Variable nucleotide G.A" 32397 / tag= aa / tag= nucleotide G.A" / note= "Variable nucleotide G.A" / tag= aa / tag= nucleotide G.A" / note= "Variable nucleotide G.A" / note= "Variable nucleotide G.A" / note= "Variable nucleotide C.T"	32406  *tage= ab  standard_name= "Single nucleotide polymorphism"  note= "Variable nucleotide C,G"
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85   AAATGCATTCTTCTACGGGATCTGGGAACTTCCAAAGCTGCCTCCTCAGAGTGGGAAT	ACCCT 271	(fir ontal ontal fises of tide files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files files	misc_feature   /*tag= b	/*tag= /*tag= /*standa /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag= /*tag=	ranne - Single nucleotide - name - single nucleotide

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18-NOV-2004 (first entry)
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ADQ97331_1
ADQ97331_2
ADQ97331_3
ADQ97331_4
ADQ97331_5
                                                                                                                                                                                                                                            Morris DW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16542 Traditricicarciaraaaradgcaraaaagroggcocococococicarocororaaric 16601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for examination of periodontal disease in which genetic polymorphisms are detected in one or more of 51 genes. The method is useful for examination, diagnosis and assessment of periodontal disease or risk of periodontal disease and the risk of its progression to severe, aggressive and chronic periodontal disease. The present sequence represents a polymorphic gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphisms associated with periodontal disease for examination and assessment of susceptibility to periodontal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCAAAGCTGGAAGTTTTTCTCTGTGACCATGGGCTAATTGGTCTCCTTCTCTGGATT
        |standard_name= "Single nucleotide polymorphism"
|note= "Variable nucleotide C,G"
|3004
                                                                                                                                                                                                                                         'standard_name= "Single nucleotide polymorphism"
'note= "Variable nucleotide A,C"
                                                                              polymorphism'
                                                                                                                                 standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide C,T"
                                                                                                                                                                                     "rd_name= "Single nucleotide polymorphism"
"Variable nucleotide G,T"
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"Variable nucleotide C,G"
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54.1%; Pred. No. 4.3;
ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 150; Opp; Japanese.
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(KAMO/) KAMOI K.
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les 73; Conserv
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misc_feature
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (1) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (GAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma arus; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (ix) as a biochip; (x) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of servinema including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 211257 BP; 55148 A; 47354 C; 46616 G; 57484 T; 0 U; 4655 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57794 CGGTGGTGATGGGCATGGGTCCTAGAGACAGCAGGCATGGGAATCAGCTCACTCCCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 CAGCGGGGGAGGCATCTTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTT
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                                                            Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.8; 1
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57854 TAGAGGAGAGTGTCTTCTCAGCTTCCT 57880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410000
510000
523643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 529; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 TCCAGAAGACTTTCTTTTCTGATTCAT
Mouse genomic sequence mCG15870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises a nucleotide sequence.
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WP Sequence split into 6 fragments
WP Fragment Name Begin
                                                                                                                                                                                                                                                                                                                   28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%;
ilarity 63.2%;
Conservative
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200001
300001
400001
                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-328604/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                       WO2003073826-A2
                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                    12-SEP-2003
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57853

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22-DEC-2003; 2003WO-US041389 27-DEC-2002; 2002US-00330773

WO2004060304-A2

22-JUL-2004

Homo sapiens

(SAGR-) SAGRES DISCOVERY

Malandro MS;

Morris DW,

WPI; 2004-543781/52

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The invention relates to human polymucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell prodiferation or cell differentiation or which may induce production of other cytokines in other cell propulations. The polymucleotides and polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 AATGGCAAAAATGGGCTTTGTTTAACGACAAATGAACTTTAATGCATGTATTTAAGAAAC 142
                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 CTTICCAGGALTCCTTTTTTTTTTTTTTTTAAAAGCCCCTTTTTCCTAAATTTAGGGATTT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 GCTTCCAACACTCAGAAGCCTATGTGAACACTCAGCCAACAAGCTGGAAGTTTTCTCT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 CTITCCAGAAGACTITCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 11764; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.4%; Score 35.2; DB 4; Length 2
Best Local Similarity 47.7%; Pred. No. 0.39;
Matches 103; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 294 BP; 100 A; 54 C; 63 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 GIGACCAIGGGCIAAIIGGICICCTICICIGGAIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genomic sequence hCG15674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN44066 standard; DNA; 99886
                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                           28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                    26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                      WPI; 2001-514838/56.
                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                             P-PSDB; AA011773
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WO200164835-A2
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                                       07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTGACCATGGGCTAATTGGTCTCCTTCTGGATTGTGGCTTATCAGATAAAAAAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 523643 BP; 156586 A; 96986 C; 101753 G; 168278 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84162 TGAĠATAĊAĠGĊAĊAGGCTTĠGĊTĊTĠAĠĊAĊATAĊĀTĊTĀAĊTĀCCAŢĠATĀTACŤĠŢĊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                              dв.
                                            Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 5.4%; Score 35.4; DB 12;
11 Similarity 48.3%; Pred. No. 12;
99; Conservative 0; Mismatches 106;
    Human cancer associated sequence HD08-032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84042 TCTAATCACAGCACATGAATTCAAT 84018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 308; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 GTGAGTCATGCCACAGGATGTCTAT 498
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Query Match Best Local Similarity

Matches

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Gaps

296

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704/c AAI91704 standard; cDNA; 294

AAI91704/ RESULT

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(first entry)

06-NOV-2001

AAI91704;

Homo sapiens

0; Gaps

Query Match 5.4%; Score 34.8; DB 11; Length 99886; Best Local Similarity 54.8%; Pred. No. 18; Matches 69; Conservative 0; Mismatches 57; Indels 0;

Search completed: August 4, 2005, 08:31:29 Job time : 435.789 secs

26083 AGGCAG 26078

This page Blonk (Usolo)

UI-R-CV1-UI-R-DO1-AL521194 BX687092 HS 3252 B 602348317

ALS21194 BX687092 BX687092 BQ1222496 BG118574 BF389719 CAK047181 N

Mus muscu BB002636 QV0-BT084 Mus muscu 602459329

BF155238 (AG534765 BG396400 BI292863 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF440523 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052 BF44052

509771 MA BP092719 398347 MA 1511 Lewi 959837 MA

BM106126 BP092719

BS2900015 UI-R-DO0-

us-09-899-276c-7.rst

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Run on:

Sequence:

Perfect

Searched:

Database

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Contact: Shaying Zhang. 190
Contact: Shaying Zhang. 190
Contact: Shaying Zhang. 190
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Guill schao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 343 row: L column: 19
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ278233 834 bp DNA linear GSS 15-OCT-2002 CH230-343L19.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-343L19, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /eex="Female"
/cell_type="Brain"
/clone_lib="CHORL-230 Segment_2"
/note="Vector: pTARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 Mbol segment Unpublished (1999)
Other_GSS9: CH230-343119.TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                    AL521194
AC627092
AC627092
AC627092
BG118574
BR3118574
BR012636
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1. .834
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CG13266 tigr-9403.

CG13266 tigr-9403.

CG13365 NDL,9403.

CG17513 AGENCOURT

CD27751 AGENCOURT

CD27755 tigr-988-

BF128774 601810241

CF895308 A0146D02-

CF895308 A0146D02-

AZZ48574 A0147H12-

AZZ48574 WHARAS4TF

BQ203820 UI-R-DNI-

CK453423 907933 MA

CK453423 907933 MA

CK453423 907933 MA

CK453423 907933 MA

EXCHORAGO UI-R-DNI-

CK453423 UI-R-DZI-

BQ210855 UI-R-DZI-

BQ199999 UI-R-DZI-

BQ1999999 UI-R-DZI-
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8064.741 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                      ggcttgtgccgagatgttcc.....aattgaatgcggtccaccaa 650
                                                                                                                                                                                                      August 4, 2005, 04:04:35; Search time 3067.89 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68479088
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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9b_htc::*;
9b_htc::*;
9b_est4:;*;
9b_est6:;*;
9b_9881:;*;
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                             score:
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Result

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Chen, D.,

GSS 02-NOV-2001

us-09-899-276c-7.rst

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Ligr-ges-dog-17000372782879 Dog Library Canis familiaris genomic, genomic survey sequence.
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2 (bases I to 673)
3 (bases I to 673)
4 (bases I to 673)
5 (bases I to 673)
7 (ctoki,Y., Watanabe,H. and Sakaki,Y.
7 (ctoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
8 (02-MG-2001)
8 (base I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke I ctoke 
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Canis familiaris
Canis familiaris
Bukaryotas, Metacoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 764)
                                                                                                                                                                                     AGU53846 673 bp DNA linear GSS 02-NOV-200:
Pan troglodytes DNA, clone: PTB-038B14.R, genomic survey sequence.
AG053846
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // organism="Pen troglodytes"
/organism="Pen troglodytes"
/mol-type="genomic DNA"
/db xxef="texon:9598"
/clone="PTB-038B14.R"
/cell_type="lymphoblast"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGCTTGTGCCGAGATGTTCCCAGCACAGCCCCATGTGAGAGCTCCCTGGC
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Pred. No. 0.66;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (chimpanzee)
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R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity 90.0%;
Matches 45; Conservative (
                          547 CAGGAGAGACTT 558
                                                                            322 ACAGTGTGÁTTT 311
                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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ZMMBBC0260N04f ZMMBBC (ECORI) Zea mays genomic clone ZMMBBC0260N04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD Calde, Panitoidaea, Andropogonee; Zea.

1 (bases 1 to 845)
Bharti,A.K., Young,S., Kaychok,S., Keizer,G., Bronzino,A.C., Schovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.

Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                     517 ATTCTATGAGGGATGCTGATATGACTAAGCCAGGAGAGACTTATTTAAAGATCTCAGCAT 576
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/lab host="E. coll DH10B"
/clone lib="ZMMBEC (ECORI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                523 TCATTATAGAATATTCTTCATGCCAGAATAATTACATAAGGTGTATTAATTGTGGA 464
                                                                                                                                                                                                                                                                                                                                                                        427 GCTAAITGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAAAAGTGAGTCATGCCA
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CHORI-230 Rat (BN/SBNHsd/MCW) BAC library produced by Pieter de Jong"
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6.5%; Score 42.4; DB 9; Length 845;
Best Local Similarity 57.6%; Pred. No. 0.54;
Matches 76; Conservative 0; Mismatches 56; Indels
                                                                                                                  Query Match 6.6%; Score 42.8; DB 8; Length 834; Best Local Similarity 54.4%; Pred. No. 0.41; Matches 86; Conservative 0; Mismatches 72; Indels
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190 Frelinghuygen Road, Piscataway, NJ 08854, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 CTTTCAGCTTGTTAACCTAGAGAAACCCGAAGCATGA 614
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/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5', genomic survey sequence.
CG856718
GG856718.1 GI:38429431
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Fax: 732 445
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                                                                                                                                    The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes,
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                        1. .764
/organism="Canis familiaris"
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/clone lib="hog Library"
/note="Site l: BstXI; Libraries were prepared from peripheral blood"
                                                    The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)
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Library was provided by David Severson
Seg primer: T7
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Tel: 301-838-3543
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8;
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Best Local Similarity 81.6%; Pred. No. 1.8;
Matches 71; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon: 1159"
/clone="NDL.94D3"
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Department of Eukaryotic Genomics
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                                                                                                                    Contact: Kirkness EF
                                                                                                                                                                                     Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@ti
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Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Musmaalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 306)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koja, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuo, Y., Makamura, M., Oda, H., Okazaki, Y., Shibata, Y., Shibata, K., Shibata, K., Shibata, Y., Shibata, K., Shibata, K., Shibata, Y., Shubata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Townoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)

L. Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 TCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCACAGGATGTC 495
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Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 TATAAGCCCATTGATTCTGGGATTCTATGAGTGATGTGATATGACTAAGCCAGGAGAGA
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                                                                                                                                                                                                                                                                                       Score 39.2; DB 8; Length 454; Pred. No. 3.9; 0; Mismatches 93; Indels
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Mus musculus
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FEATURES

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/mol_type="mRNA"
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/clone="Thefe:30922965"
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
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1 (bases 1 to 569)

1 (bases 1 to 569)

1 (bases 1 to 569)

2 (cle,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pepe,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Khiter,E., Bennett,J., Franklin,C., Tasgareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R. Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Toxoplasma EST Project

Toxoplasma EST Project

Washington University School of Medicine
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TGESTZY123e02.y1 TGMAS Tachyzoite CDNA Library Toxoplasma gondii
CDNA clone TGESTZY123e02.y1 5', mRNA sequence.
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Fax: 314 286 1810
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Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
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55.2%; Pred. No. 7.1;
tive 0; Mismatches 60; Indels (
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM1163 row: a column: 22 High quality sequence start: 3 High quality sequence start: 3 High quality sequence.
                                                                                                                                                               ity sequence stop: 361.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                        High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rml0A07 Behbesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mary Hendrix
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llarity 51.1%; Pred. No. 4.5;
Conservative 0; Mismatches 87; Indels C
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/mol_type="mRNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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                                                                                                                                              Length 636;
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                                                                                                                                              Query Match 5.8%; Score 37.6; DB 9;
Best Local Similarity 49.5%; Pred. No. 13;
Matches 97; Conservative 0; Mismatches 99;
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Pred. No. 18;
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                                                                                                                                                                                             /db xref="taxon:5811"
/clone="TgESTzyi23e02.y1"
/dev stage="Tachyzoite"
/dev stage="Tachyzoite"
/lab host="ElectroTen Blue cells (Stratagene)"
/clone_lib="TgMAS Tachyzoite cDNA Library"
/clone_lib="TgMAS Tachyzoite cDNA Library"
/note="Vector: pBluegcript II SK+; Site 1: EcoHI; Site 2:
Xho1; The cDNA library was constructed by Keliang Tang,
and Robert Cole at Washington University. cDNA was
synthesized from Poly(A) + mRNA using an oligo-d(T) primer
containing a Xho1 site. Following second strand synthesis,
EcoRI adapters were ligated to the cDNA, and products were
size-selected on sephacryl S500. The cDNA were
directionally cloned into the EcoRI/Xho1 prepared
pBluescript II SK+ vector, and electroporated into
ElectroTen Blue cells (Stratagene). The library may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tigr-ges-dog-17000327371506 Dog Library Canis familiaris genomic, genomic survey sequence.
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Cockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AGACTITCTITICTGAITCATACCCTTCACCTTCCCTGTGTTACTGTCTGAIATATATGCA 305
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.

1 (bases 1 to 616)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 37.8; DB 6; Length 569; 60.0%; Pred. No. 11; ive 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 AAGGCCAAGTCACTTTCCAGAGATGACAACTCCTTCCTGAAGTAG 350
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/organism="Toxoplasma gondii"
/mol type="mRNA"
/strain="Tachyzoite"
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
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Location/Qualifiers
                    -40RP from Gibco
                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contaminants."
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Best Local Similarity 60.0%
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/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: Not1; Mouse cDNA project by the Laboratory of GeneTics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgaun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were obtained from Dr. Kenneth R. Boheler (National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukamalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 640)
1 (bases 1 to 640)
1 (bases 1 Lo 1,m.M.K. and Ko.M.S.H.
Construction of long-transcript enriched cDNA libraries from submigrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF895446 11near EST 04-NOV-2003 A0147H12-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1) Mus musculus cDNA clone NIA:A0147H12 IMAGE:30728159 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                          561 AGTÍCTÍGITIGCÍÁCÁTGÁGÁCÁACCACÁATCÁTÍCTACCAÁGÁTGTCTCCÍTTAÍCAAT 620
and cloned into Sall/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao."
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Laboratory of Genetics
Mational Institutes of Health
Mational Institute on Aging/National Institutes of Health
Maisonal Institute on Aging/National Institutes
MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Blate: All 7 row: H column: 12
Seg primer: M13 Reverse
High quality sequence stop: 640
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/organism="MRNA"
/mol_type="mRNA"
/strain="129/Sv x 129/Sv-CP"
/db_xref="niasST:A0147H12-5"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                     ; Score 37.4; DB; Pred. No. 15; 0; Mismatches
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Mus musculus
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Local Similarity 54.8%;
hes 74; Conservative C
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Site 1: Sall;
Site 2: Noctor: DCMV-SPORT6 (Invitrogen); Site 1: Sall;
Site 2: Noctor: DCMV-SPORT6 (Invitrogen); Site 1: Sall;
Site 2: Noctor: DCMV-SPORT6 (Invitrogen); Note;
Genetics, National Institute on Aging (NIA), Intramaral
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were obtained from Dr. Kenneth R. Boheler (National
Institute on Aging, USA). ES cells were cultured without
feeder cells in the presence of LIF and BRL-conditioned
media. Double-stranded cDNAs were synthesized with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 637). Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF895308 637 bp mRNA linear EST 04-NOV-2003 A0145D02-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1) Mus musculus CDNA clone NIA:A0146D02 IMAGE:30728005 5', mRNA
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                                                                                                   188 GAGGGCATCTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTTTCCAGAAG 247
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/mol type="mRNA"
/mol type="mRNA"
/strafi="129/$x 129/$v-CP"
/db xref="taxon:10090"
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National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Bmail: cana@lgsun.grc.nia.nih.gov
Plater: A0146 row: D column: 02
Seq primer: M13 Reverse
High quality sequence stop: 637
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                                                Mismatches
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                                                   Conservative
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CF895308
                                                      Matches
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/note="Organ: Kidney/Brain, Vector: pBACe3.6; Site_1:
EcoRI, Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU224166 655 bp mRNA linear EST 26-NOV-2002
603799875F1 CSEQCHN23 Gallus gallus cDNA clone ChEST769f20 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AGACAGCTGTCACTTTCCAGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 AGAGAATTGTAAATTGAAGGAATAATTCTGCTTTTTCTCTTTCTCTTCTTCGTTCCATAC 485
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, J. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.8%; Score 37.4; DB 8; Best Local Similarity 54.8%; Pred. No. 15; Matches 74; Conservative 0; Mismatches 61;
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/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Gallus gallus"
                                    'organism="Mus musculus"
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Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                      /db_xref="taxon:10090"
/clone="RPCI-23-93C11"
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/lab_host="DH10B"
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E 1 (bases 1 to 644)
S Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Lupublished (1999)
Diptrophished (1999)
Cother GSSs: RAPIG Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library PCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html
Plate: 93 rows. C column: 11
Seg primer: SP6
Class: BAC ends.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 644)
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Matches 74; Conservative
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DEFINITION RESULT 13 AZ248574

ACCESSION VERSION KEYWORDS SOURCE

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COMMENT

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/note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed_from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI; size-selected, and cloned into the NotI and EcoRI compatible sites of a custom medified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
22709111
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Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Volik SV
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Ex 0808, San Francisco, CA 94143-0808, USA
Tel: 415 SO2 7666
Fax: 415 SO2 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
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/organiam="Homo sapiens"
/mol_type="genomic DNA"
/db_Xref="taxon:9606"
/clone="MCF7_l-7111"
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                           /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
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                                                                                                                                 Length 725;
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                                                                                                                                 5.8%; Score 37.4; DB 8;
49.2%; Pred. No. 16;
tive 0; Mismatches 101;
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/sex="female"
                                                                                                                                        Query Match
Best Local Similarity 49.2
Matches 98; Conservative
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Sequence 273, App
Sequence 1, Appli
Sequence 1, Appli
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Sequence 15851, A
Sequence 15852, A
Sequence 12387, A
Sequence 12724, A
Sequence 12724, A
Sequence 17726, A
Sequence 17490, A
Sequence 16539, A
Sequence 16639, A
Sequence 16639, A
Sequence 17490, A
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Sequence 2294, App
Sequence 17434, App
Sequence 13915, A
Sequence 14, Appl
Sequence 160628,
Sequence 171536,
Sequence 2476, Appl
Sequence 2786, Appl
Sequence 2786, Appl
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1788, Ap
16240, A
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Sequence 16944, A
                                                                                                                  August 4, 2005, 07:01:49; Search time 133.947 Seconds (without alignments) 7940.282 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/RECOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-949-016-15851
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Sequence 94, Application US/09220132
Sequence 94, Application US/09220132
Patent No. 6506607
BATEL NO. 6506607
BATEL NO. 6506607
BATEL NO. 6506607
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US 60/079,303
PRIOR PAPLICATION NUMBER: US 60/079,303
PRIOR PAPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NOS: 191
Sequence 16600, A Sequence 2613, Ap Sequence 663, App Sequence 663, App Sequence 15238, A Sequence 17504, A Sequence 17504, A Sequence 13909, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 1118, A Sequence 11805, A Sequence 11805, A Sequence 11805, A Sequence 11805, A
                                                                                                                                                           Sequence 13118, A Sequence 11809, A Sequence 34983, A Sequence 154033, Sequence 16, Appl Sequence 1987, Ap Sequence 17185, A
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US-09-949-016-16600
US-09-949-016-16073
US-08-621-978-1313
US-08-956-1718-663
US-09-949-016-15218
US-09-949-016-15218
US-09-949-016-15211
US-09-949-016-17204
US-09-949-016-1719
US-09-949-016-1719
US-09-949-016-1719
US-09-949-016-1719
US-09-949-016-1719
US-09-949-016-1718
US-09-949-016-1718
US-09-949-016-1718
US-09-949-016-34983
US-09-949-016-34983
US-09-949-016-34983
US-09-949-016-34983
US-09-949-016-34983
US-09-949-016-34983
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19.4%; Pred. No. 0.085;
tive 90; Mismatches 109;
                                                                                                                                                                                                                                                                                            AL I GNMENTS
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; OTHER INFORMATION: n = A,T,C or
US-09-220-132-94
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nes 48; Conservative
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385136
832
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143640
187848
16404
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116425
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NAME/KEY: misc_feature
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   NNNNNNN44444444444
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ORGANISM: Human
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Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

SEREMAL INFORMATION: Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERRACE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15852

LENGTH: 205044
Sequence 15631, Application US/09949016

| Sequence 15651, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| TITLE OF UNIVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| PRIOR PELLING DATE: 2000-04-14
| PRIOR PILING DATE: 2000-10-20
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTHARE: FREESE FOR WINDOWS VETSION 4.0
| SEQ ID NO 15881
| LENGTH: 205044
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S.6%; Score 36.2; DB 4; Length 205044;
Best Local Similarity 53.1%; Pred; No. 2.6;
Matches 77; Conservative 0; Mismatches 68; Indels 0;
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851
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       US-09-949-016-15851/c
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ORGANISM: Human
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US-09-949-016-15853/C

| Sequence 15853, Application US/09949016
| Sequence 15853, Application US/09949016
| Sequence 15853, Application US/09949016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| PRIOR PLILING DATE: 2000-04-14 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-00-09-08 |
| PRIOR PILING DATE: 2000-00-09-08 |
| WUMBER OF SEQ ID NOS: 207012 |
| SOFTHARE: ESSECTE FOR WINDOWS VERSION 4.0
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                                                                                                            Length 205044;
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                                                                                                               Query Match
5.6%; Score 36.2; DB 4;
Best Local Similarity 53.1%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches 68;
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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; LOCATION: (1)...(205044);
.CTHER INFORMATION: n = A,T,C or G
US-09-949-016-15853
; LOCATION: (1) ... (205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852
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US-09-949-016-12387/c
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Sequence 12725, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: PRESERQ for Windows Version 4.0
                                                                                                                                                       3176 TATCTGCTGGCGCTGAAATTCTCTCAGGACAGCTCAGCCCTGCTTTCCAGAAGATGAGAG 3117
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                                                               3236 ccangegeccegesasangerescaacanaesnecareasasasesesacrescececereca 3177
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Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Gloradno, J. Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725
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US-09-949-016-12725/c
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US-09-621-976-15639
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 12725
LENGTH: 223471
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1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/0949016

1S-GGREAL INFORMATION: WITH HOMEN DISEASE, METHODS OF DETECTION AND USES THEREOF

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 CURRENT FILING DATE: 2000-04-14

1 PRIOR PLILING DATE: 2000-10-20

1 PRIOR PELICATION NUMBER: 60/231,768

1 PRIOR PLILING DATE: 2000-10-03

2 PRIOR APPLICATION NUMBER: 60/231,498

2 PRIOR PLILING DATE: 2000-09-08

3 NUMBER OF SEQ ID NOS: 207012

4 SOFTHARE: PRESERE FOR WINDOWS VERSION 4.0

5 SEQ ID NO 12724

1 LENGTH: 223471
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION WINBER: 60/241,755
PRIOR PELLING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSO FOR WINDOWS VERSION 4.0
SEQ ID NO 12387
LENGTH: 223471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3176 TATCTGCTGGAGCGCTGAAATTCTCTCAGGACAGCTCAGCCCTGCTTCCAGAAGATGAGAG 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 223471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
5.6%; Score 36.2; DE
Best Local Similarity 53.1%; Pred. No. 2.8;
Matches 77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3116 GACTTCACAAGCTGCCCACTGCCA 3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 GGAGGCAGACAGCTGTCACTTTCCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | NAME/KEY: misc_feature
| LCCATION: (1)...(223471)
| CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12387
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724
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LOCATION: (1)...(22347)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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48.78;

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Local Similarity 48.7
les 92; Conservative
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 GACAGAGCAGAAGTGGG-----AGGCAGACAGCTGTCACTTTCCAGAAGACTTTCTTTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATACGAAAGGCCAAGTCAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITICCAGAGATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 YAMMSMWCARMACAMAGMRSAWWKCSRAKYMYMAKSCMYCAKWSCSARSAKCGRSCCTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGAACACTCAGCCAGCAAAGCTGGAAGTTTTTCTCTGTGACCATGGGCTAATTGGTCT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 CAAATGCATTCTTCTACGGGATCTGGGAACTTCCAAAGCTGCCTCCTCAGAGTGGGAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 CTYKKSYYTCRKSYYTYRISTSKKGMGTKKSRWSYTWSNKSYTWGCSKKWKRMYWSAGAW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 YGSKGMSCKGSRSKYYGSWKMYYGKYTMCTSKYKSSKMSYKKSSMCYTYMMCYYTYWWCT
                                                                                                                                                                                                                                                                                                                                                                         24 CACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCCAGTATCTGGAATGCAGGCTCCAGC
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                                                                                                                                                                                                                                                                                                        'n,
                                                                                                                                                                                                                           Query Match 5.5%; Score 35.6; DB 4; Length 505; Best Local Similarity 14.3%; Pred. No. 0.096; Matches 65; Conservative 181; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 CCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAG 474
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1) ... (141115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17490
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                                                                                        TYPE: DNA
COGANISM: Homo sapiens
US-09-621-976-15639
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ORGANISM: Human
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                       SEQ ID NO 15639
LENGTH: 505
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GENERAL INCORMATION:
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA-0041 US
CURRENT PILLIA DAPLICATION NUMBER: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
                                                                                                                17485 ICICTITATGIAGTIAGIGGCTIGIAAGCTGTCAACTTGIAAAIGATGCCGTTGGAAATT 17544
                                                                                                                                                                                                                                                                                                                            17605 ATTAGGTCAAGATGTGTAAGACCTGTATACTGAGAACTATGATATATTGCTCAGAGAAAT 17664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wright, David A.
APPLICANT: Wright, David A.
TITLE OF INVENTION: PLANT RETROBLEMENTS AND METHODS RELATED THERETO
FILE REPERENCE: P-10652
CURRENT APPLICATION NUMBER: US/09/586,106D
CURRENT APPLICATION NUMBER: 60/087,125
PRIOR APPLICATION NUMBER: 60/087,125
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastERQ for Windows Version 4.0
SOFTWARE: PastERQ for Windows Version 2.0
                                                                    436 TCTCCTTCTTGTGGGTTATCAGATAAAAACAAGTGAGTCATGCCACAGGATGTC
                                                                                                                                                                       TATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCCAGGAGAGA
                                                                                                                                                                                                                                                                             556 CTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCCGAAGCATGAC
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Pred. No. 14;
0; Mismatches
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; Patent No. 6720479
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9%;
Matches 72; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                              616 TGGATTATA 624
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US-09-586-106D-106
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                       NAME/ALT: m18C TEALULE
LOCATION: (148948). (148948)
OTHER INFORMATION: n equals a, t,
MAME/KET; misc. feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t,
MAME/KET; misc. feature
LOCATION: (191989). (191989)
OTHER INFORMATION: n equals a, t,
MAME/KET; misc. feature
LOCATION: (191989). (191989)
OTHER INFORMATION: n equals a, t,
MAME/KET; misc. feature
LOCATION: (191955). (191995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (234220)...(234220)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (309398)...(309398)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (309348)...(309348)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (309418)...(319318)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (312837)...(312837)
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LOCATION: (231980) .. (231980)
OCHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234187) .. (234187)
OTHER INFORMATION: n equals a, t,
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LOCATION: (319226). (319226)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (559167). (559167)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (559241). (559241)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (600922). (600922)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (600922). (600922)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (622708). (622708).
                               OTHER INFORMATION: n equals a,
                                                   NAME/KEY: misc_feature_LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
THER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
                                                                                                                       NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORWATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals
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LOCATION: (713652)..(713652)
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APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii
FILE REFRENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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; OTHER INFORMATION: Incyte ID No. 6673549 404601.11

; NAME/KEY: unsure

; LOCATION: 1731, 1736, 1739, 1742-1743, 1749, 1751-1752, 1754, 1756

US-09-976-594-273
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                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                               Query Match
5.1%; Score 33.4; DB 4; Length 1759;
Best Local Similarity 55.7%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 51; Indels 0
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or
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LOCATTON: (98239). (98239)
OCTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
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LOCATION: (28257)..(28258)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
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ORGANISM: Methanococcus jannaschii
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 273
                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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RESULT 13
US-09-692-570-1/c
; Sequence 1, Application US/09692570
; Sequence 1, Application US/09692570
; Batent No. 6797466
; GENERAL INFORMATION:
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco.; Patent No. 6797466
; TITLE OF INVENTION: Januaschii
; TITLE OF INVENTION: Januaschii
; FILE REPERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT PILING DATE: 1996-08-22
; PRIOR FILING DATE: 1996-08-22
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1.
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NAMES/KEY: misc_feature
LOCATION: (148948)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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LOCATION: (98343)..(98343)
JTHER INFORMATION: n equals
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LOCATION: (163385)..(163385)
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (98266)..(98
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263225 TCAGAAATGCATCCCCAACCTGAACACTTGGCCTTTCTTCCTCACT 263179
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; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals a, t, C,
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LOCATION: (1130881). (1130881)
COTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (1310988). (1310988)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (1313224). (1313224)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1084830). (1084830)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
                                NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a,
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LOCATION: (1637998) .. (1637998)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
               INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (1569020)..(1569020)
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263285 TTCATAGCTTTAACTTTTCCTGTTTTTTACTGCCTCTAAAACAGCATCAATTAAACATTTT 263226 262 ITCATACCCTTCACCTTCCCTGTTTTACTGTCTGATATATGCAAAGGCCAAGTCACTTT 321 Gaps DB 4; Length 1664976; 263225 rcagaaargcarccccaaccrcaacerregccrrrcrrcrcacr 263179 ö 322 CCAGAGATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACT 5.1%, Score 33.4, D 57.0%, Pred. No. 91; tive 0; Mismatches FEATURE:
NAME/KEY: misc\_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g g b ör or ö ÖĽ or ö ö ö ö ö ö or c, or ů NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, c, RESULT 14 US-09-640-211A-154 ; Sequence 154, Application US/09640211A ů ϋ ບັ NAME/KEY: misc feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, t, ú NAME/KEY: misc feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (855539)..(855539) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1084830)..(1084830) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1096846)..(1096846) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (779455)..(779455) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (871519)..(871619) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1130881)..(1130881) OTHER INFORMATION: n equals a, CALLURE:
NAME/KEY: misc\_feature
LOCATION: (741684)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (713652)..(713652) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (779576)..(779676) OTHER INFORMATION: n equals Query Match
Best Local Similarity 57.0
Matches 61, Conservative g ઠે ద ઠે

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Sequence 16944, Application US/09949016

Sequence 16944, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOU3307

CURRENT APPLICATION WUMBER: 60/241,755

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: PEBESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114230 GCTCACCCTCGGTGGTTGTTGCACCATACCCAAAACCAAGGGGCAGAAAGGTGGTGAAGATGT 114289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 GGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAACAAGTGAGTCATGCCACAGATG
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Pred. No. 21;
0; Mismatches 108; Indels 0;
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5.1%; Score 33.2; DB 4; Length 1144;
Best Local Similarity 55.1%; Pred. No. 1.1;
Matches 65; Conservative 0; Mismatches 53; Indels 0.
            GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT PILNG DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2268
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154
LENGTH: 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.6%;
Matches 98; Conservative (
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16944
6833446
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US-09-949-016-16944
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LENGTH: 121384
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Qy 614 ACTGGATTATAAAGGGAAATTGAATG 639
Db 114410 CCAACATTAGAAACTGAATTTCAATG 114435
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Search completed: August 4, 2005, 14:41:07 Job time: 142.947 secs

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US-09-899-276-7
                                                                                                                                                                                     August 4, 2005, 08:04:16; Search time 1159.47 Seconds (without alignments) 3633.986 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB. Beq:*
/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB. Beq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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650
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Description							Sequence 94, Appl
COLUMNIA			ID	9 US-09-899-276-7	US-10-685-705-4	US-10-685-705-3	US-10-311-455-1626	US-10-311-455-1625	US-10-311-455-973	US-10-831-704-94
			В	6	19	19	15	15	15	21
		Query	Length	650	11793	3221	5926	5926	6557	1497
	de	Query	Match	100.0	94.9	93.6	61.8	56.2	5.9	5.6
			Score	650	616.6	608.6	401.8	365.4	38.2	36.6
		Result	No.	1	7	c	Ω	2	9	7

95,44	2146 9465, 9465, 9465, 1023 1023 11233
10-027-632-2543 10-027-632-2543 10-027-632-2543 10-027-632-2543 10-027-632-2543 10-027-632-2543 10-027-632-2543 10-027-632-2549 10-027-632-1056 10-027-632-1056 10-027-632-1056 10-027-632-1056 10-027-632-1506 10-027-632-1506 10-027-632-1506 10-027-632-1506 10-027-632-1506 10-027-632-1506	US.10-767-701-14649 US.10-221-613-219 US-09-938-842A-465 US-09-938-842A-465 US-10-311-455-984 US-10-108-260A-301 US-09-876-143-474 US-10-311-455-711 US-10-221-613-89 US-10-221-613-89 US-10-239-607-106 US-09-938-842A-1023 US-09-938-842A-1023 US-09-938-842A-1023 US-10-311-455-1294 US-10-318-934-191
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1266 1266 1266 1266 1266 1266 1266 1319 1319 1319 671 671 671 671 689 926 926 926 928	13576 19576 19576 19576 19576 19573 1959 1959 1959 1959 1959 1959 1959 195
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## ALIGNMENTS

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APPLICANT: Rost, Frank
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Covi, Johannes
APPLICANT: Covi, Johannes
APPLICANT: Poustka, Annemarie
APPLICANT: Poustka, Annemarie
APPLICANT: Patzelt, Andrea
APPLICANT: Patzelt, Andrea
APPLICANT: Patzelt, Andrea
APPLICANT: Patzelt, Andrea
APPLICANT: Patzelt, Andrea
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APPLICANT: Patzelt, Andrea
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100.0%; Score 650; DB 9; Length 650;
Best Local Similarity 100.0%; Pred. No. 1e-209;
Matches 650; Conservative 0; Mismatches 0; Indels
; Sequence 7, Application US/09899276
; Patent No. US20020106355A1
; GENERAL INFORMATION:
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US-09-899-276-7
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Sequence 4, Application US/10685705
Publication No. US20040177387A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF Kentucky Research Foundation
APPLICANT: UNIVERSITY OF Mubbati
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT APPLICATION NUMBER: 60/422,096
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR SED ID NOS: 10
NUMBER OF SEQ ID NOS: 10
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Score 616.6; DB 19; Length 11793;
Pred. No. 1.2e-197;
0; Mismatches 14; Indels 1; (
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al Similarity 97.7%;
636; Conservative
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CORGANISM: Homo sapiens
US-10-685-705-4
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LENGTH: 11793
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Best Local 8
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Sequence 3, Application US/10685705

Sequence 3, Application US/10685705

Sublication No. US2040177387A1

Sublication No. US2040177387A1

SERERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University Ambati
TITLE OF INVENTION: Degeneration
TITLE OF INVENTION: Degeneration
TITLE OF INVENTION: Degeneration
TITLE OF INVENTION: Degeneration
FILE REPERENCE: 105029-0415
CURRENT APPLICATION NUMBER: 05/10/685,705
CURRENT FILING DATE: 2003-10-16
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10

SOFTWARE PARENCE: Patentin version 3.2
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AAGCTGCCTCCAGAGTGGGAATTTCCACTCACTCTCACGCCAGCACTGACCTCC
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Pred. No. 3e-195;
0; Mismatches 14; Indels 1;
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Best Local Similarity 97.7%;
Matches 628; Conservative
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ORGANISM: Homo sapiens
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US-10-311-455-1625
US-10-311-455-1625
Sequence 1625, Application US/10311455
Publication No. US20030143606A1
Sequence 1625, Application US/10311455
Publication No. US20030143606A1
SEREMAL INFORMATION:
APPLICANT: DIEFENNECK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Oytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DT/EP01/0737
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
LENGTH:: 5926
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                      ATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCAAA
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1625
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ORGANISM: Artificial Sequence
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Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIREPRENECK, Christian

APPLICANT: BERLIN, Kurt

ITLE OF INVENTION: Cytosine methylation

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

WHICH FILING DATE: 2000-09-01

WHICH FILING DATE: 2000-09-01

ERNOR FILING DATE: 2000-09-01

LENGTH: 5926
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                  CTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTGTATATGCAAAG
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; OTHER INFORMATION: chemically treated genomic DNA
US-10-311-455-1626
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US-10-311-455-1626/c
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US-10-831-704-94

US-10-831-704-94

Sequence 94, Application US/10831704

Publication No. US20050100931A1

GENERAL INFORMATION:

ABPLICATION:

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND

TITLE OF INVENTION: ASSESSMENT

TITLE OF INVENTION: ASSESSMENT

TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE

TITLE OF INVENTION: ASSESSMENT

TITLE OF INVENTION: US/10/10/81,704

CURRENT APPLICATION NUMBER: US/10/155,653

PRIOR PRILING DATE: 1998-12-23

PRIOR PILING DATE: 1998-12-23

PRIOR FILING DATE: 1998-12-23

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 191

SEQ ID NOS: 191

SEQ ID NOS: 191

SEQ ID NO 94

SEQ ID NO 94

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SEQ ID NO 94

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SEQ ID NO 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 CAGGAGACTTATTTAAAGAICTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 gaggirgaggirahagggagirgagarrahaharharrgrafraraggringggagggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 Grégaratrigráárttraketratrirtgéaagtriagéragéagaarcertréagtriég 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCCAGTATCTGGAATGCAGGCTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      427 gcraarregretectrecregarreregerrateagaraaaaacaagreagecea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 CAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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ORGANISM: Artificial Sequence
FERATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KES: 5.004
LOCATION: 5.004
GOTHER INFORMATION: n is a or g or c or t
US-10-311-455-973
                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                      Length 6557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 36.6; DB 21; Length
; Pred. No. 0.59;
90; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                          Score 38.2; DB 15;
Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          607 AAGCATGACTGGATTATAAAGGGAAATTGAA 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 GAGATTTTGTTTTAAAAAATAAAAAAAAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(1497)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 19.4%;
Matches 48; Conservative 90
                                                                                                                                                                                                                                                                                                                    Query Match 5.9%;
Best Local Similarity 48.8%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-831-704-94
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Use of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DC/EPO1/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 973
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCAGGCCAGCACTGACCTCCC 180
                                                                                                                                                                                                                                                                                                                                     GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTTCTACGGGATCTGGGAACTTCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 ACTAAGCCAGGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGAAGACTTTCTTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 AAACCCGAAGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
                                                                            Length 5926;
                                                                                                                                              1;
                                                                                                                                          Indels
                                                                                   Score 365.4; DB 15;
Pred. No. 2.1e-112;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 973, Application US/10311455 publication No. US20030143606A1 GENERAL INFORMATION:
                                                                                   Query Match 56.2%;
Best Local Similarity 73.6%;
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-311-455-973
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159 CTCACGCCAGCACTCCCCAGCGGGGGGGCATCTTTCTTGACAGAGCCAGAAGTG 218
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 12000-02-24
PRIOR FILING DATE: 1999-09-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-08
PRIOR FILING DATE: 1999-08-08
PRIOR FILING DATE: 1999-08-08
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 354389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.2; DB
Pred. No. 0.73;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/199,483
PRIOR PELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 GGAGGCAGACAGCTGTCACTTTCCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GACTTCACAAAGCTGCCCACTGCCA 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 254389, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.1%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-027-632-254389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-027-632-254388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 254388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
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                                                                                        TICCACTCACTTCTCTCACGCCAGCACTGACCTCCCAGCGGGGGGGCGCATCTTTTCTTG 204
                                                                                                                                                                                     781 CCATGGGGCCGGGGAGGTGGCAACATAGGTGCATGAGAGGGGGGACTGCCCCCACCCTGCA 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 254387, Application US/10027632
Fublication No. US2020198371A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
FILE REFERENCE: 2002-04-30
FILE REFERENCE: 2000-07-12
FRING DATE: 2000-07-12
FRING DATE: 2000-07-12
FRING DATE: 2000-07-20
FRING PAPLICATION NUMBER: US 60/198,676
FRING PAPLICATION NUMBER: US 60/198,676
FRING PAPLICATION NUMBER: US 60/198,676
FRING PAPLICATION NUMBER: US 60/198,676
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FRING PAPLICATION NUMBER: US 60/198,676
FRING PAPLICATION NUMBER: US 60/198,676
FRING PAPLICATION NUMBER: US 60/198,638
FRING PAPLICATION NUMBER: US 60/185,218
FRING PAPLICATION NUMBER: US 60/167,363
FRING PAPLICATION NUMBER: US 60/167,363
FRING PAPLICATION NUMBER: US 60/167,363
FRING PAPLICATION NUMBER: US 60/167,363
FRING PAPLICATION NUMBER: US 60/167,363
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FRING PAPLICATION NUMBER: US 60/167,363
FRING PAPLICATION NUMBER: US 60/167,363
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Sequence 254389, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: POLYMOCYPHISMS in the Human Genome

FILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254387
LENGTH: 1266
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68; DB 13;

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ORGANISM: Human
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CURRENT FILING DATE: 2002-04-30
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1900-09-28
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-01-88
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PRIOR PELING DATE: 1999-01-88
PRIOR PELING DATE: 1999-01-89
PRIOR PELING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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5.6%; Score 36.2; DB 13; Length 1266;
Best Local Similarity 53.1%; Pred. No. 0.73;
Matches 77; Conservative 0; Mismatches 68; Indels 0;
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  Length 1266;
                                           Indels
219 GGAGGCAGACAGCTGTCACTTTCCA 243
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US-10-027-632-254390
; Sequence 254390, Application US/10027632
; Publication No. US20020198371A1
      Query Match
Best Local Similarity
Matches 77; Conserv
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RESULT 12
US-10-027-632-254387
; Sequence 254387, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

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US-10-027-632-25438B

Jegupence 254388, Application US/10027632

Jegupence 254388, Application NO. US20030204075A9

Jebulication No. US20030204075A9

Jebulication No. US20030204075A9

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILER REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
CURRENT APPLICATION NUMBER: US/10/27,632
CURRENT APPLICATION NUMBER: US 60/18,676
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PAPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-103-28
PRIOR FILING DATE: 1999-103-28
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Publication No. US20030204075A9

Publication No. US20030204075A9

Fubrication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: DATE: 108027.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

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PRIOR FILING DATE: 2000-02-24

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PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-10-28

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Pred. No. 0.73;
0; Mismatches 68;
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Best Local Similarity 53.1%;
Matches 77; Conservative
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Best Local Similarity 53.1;
Matches 77; Conservative
                      ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254388
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AC096195 Rattus no
AX343337 Sequence
AX343328 Sequence
AX143328 Sequence
AF19531 Homo sapien
AF19531 Homo sapien
AC105549 Homo sapien
AC105549 Homo sapien
AC10355 Rattus no
AC103285 Rattus no
AC103285 Rattus no
AF510258 Human res
BT005812 Arabidops
AY094410 Arabidops
AY094410 Arabidops
AX025126 Homo sapiens
AK025126 Homo sapiens
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Mus musculus chromosome 12, clone RP23-36H21, complete sequence.
AC121286
AC121286.7 GI:45237272
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roesl,F., Soto,U., Coy,J., Finzer,P., Delius,H., Poustka,A., zur Hausen,H. and Patzelt,A. Regulatory sequences of the human mcp-1 gene Patent: EP 1170372-A 8 09-JAN-2002; DebursCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS (DE)
                                                                                                                                                                                                                                                                                                                                                                  Procavia
S.pombe c
Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA

    .20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_raref="taxon:32630"
    /note="Description of the Artificial Sequence: Part of 3'-DHSR"

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Pred. No. 23;
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Sequence 8 from Patent EP1170372.
AX343335 GI:18491685
                    AC095195
AC096479
AC096479
AC343337
AF519531
HFY18933
AC005549
AC137407
AC129164
AC12285
BT01285
BT013955
AF510258
BT013955
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AC10385
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AL138813
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85.0 245273
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AUTHORS
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JOURNAL
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LOCUS
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AC1016406 MUB MUSCU
AC004259 HOMO SADI
AC009899 HOMO SADI
AP001356 HOMO SADI
AF071772 MUB MUSCU
AC021802 HOMO SADI
AC133524 MUS MUSCU
AC026086 HOMO SADI
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AC087482 HOMO SADI
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AC125890 RATUS NO
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                                                                                                                                                                                                                                                                                                                                                                  9416466
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovitc, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Street, Cambridge, MA. O2141, USA on Mar 6, 2004 this sequence version replaced gi:41058341.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L22843
Center clone name: 36_H_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23 Female Mouse BAC"
1. .2223
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Web site: http://www-seq.wi.mit.edu
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1693. 1786
/rpt family="T-rich"
complement (1787. 1926)
/rpt family="B1 hM"
complement (1966. 2095)
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clone_end:SP6"
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10331. 10380
/rpt_family="(CCCCCA)n"
10553. 10629
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="12"
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2224. .220
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clone end:SP6
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6179...6226
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022. .7068
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6981. .7019
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3892. .4400
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Birren, B., Lintcon, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bacasien, V., Bloom, Y., Chang, J., Bouchstavity, L., Anderson, S., Barna, N., Barna, N., Bouchstavity, L., Anderson, S., Barna, N., Canagelo, M., Collins, S., Collymore, A., Chang, J., Boukhaller, E., Grover, P., Petzlang, W., Callins, S., Collymore, A., Cooke, P., Petzlang, W., Calma, J., Canagelo, D., Calagan, J., Caradya, S., Gord, S., Goyete, M., Mille, W., Lindblad-Toh, K., Liu, G., Landerse, R., Landerse, R., Landerse, R., Landerse, R., Machan, D., Canad, P., Machan, D., Canad, P., K., Liu, G., Mactien, R., Major, J., Marquis, M., Marcan, C., McCarthy, M., McBwan, P., McKernan, K., Maldrim, J., Meneus, L., McCarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., Spolanovic, N., Stonaer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Sch
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L. Submitted (22-JAN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 227648)

Birren, B., Wubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, M., Bastien, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Boguslavkly, L., Cook, A., Cook, A., Cook, B., Cornis, B., Dearellano, K., Cook, A., Cook, A., Cook, M., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Hagopian, D., Uohnson, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Machen, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Machen, C., Maclathy, M., Maldrim, J., Meneus, L., Minova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 227648)
                                                                                                                                                                      Birren, B., Nusbaum, C. and Lander, B.
Mus musculus chromosome 12, clone RP23-36H21
Unpublished
                             Mus musculus (house mouse)
Mus musculus
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Colangelo, M., Campopiano, A., Chang, J., Chagaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Caok, P., DeArellano, K., Dewar K., Diaz, J. S., Dodge, S., Farco, S., Perreira, P., FitzHugh, W., Gage, D., Galagan, J., Gard, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Marchie, W., Ildevil, Johnson, R., Jones, C., MacCarhy, M., McEwan, P., McKernan, K., Malcdim, J., Menteus, L., Minova, T., Manga, V., Murphy, T., Naylor, J., Nayton, C., Noran, C., Noran, C., Noran, C., Pornor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Stantos, R., Schauer, S., Schupback, R., Stantos, S., Severy, P., Spencer, B., Stanger, Theadare, J., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers,
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Direct Summission

Submitted (12-SEP-203) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

E S (bases 1 to 234354)

E S (bases 1 to 234354)

S Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Andchchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Cooke, P., Carum, B., DeArellano, K., Cooke, P., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farckson, J., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Garban, L., Grand-Pierre, N., Haime, W., 114cv, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., Maccarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Major, J., Manning, J., Matthews, C., McCarthy, M., Wajor, J., Mathova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
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4. (bases 1 to 234354)
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Mus musculus chromosome 3, clone RP23-427K12, complete sequence.
AC116406
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 3, clone RP23-427K12
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/rpt_family="B1_MM" complement(13583. .13648)
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complement (14121. .14515)
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14519. .14624
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12843. .12926

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12843. .12926

/rpt_family="(TTCTC)n"

/rpt_family="Lx"

/rpt_family="Lx"

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complement(13334..13478)
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complement(13561..13582)
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complement(13665, .13725)
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13779, .1380
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18107. .18757
/rpc_family="LIMAS"
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19079. .19134
/rpt_family="(GA)n"
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2159. .12198
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                   10646. .10898
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11949. .11975
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/rpt_family="L1"
13295. .13321
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Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
                                                                                          Submitted CT-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Cn Sep 12, 2003 this sequence version replaced g1:33413361.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L23945
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complement(11155..11513)
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2895. .3003
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complement(8362. .8647)
rpt_family="B4A"
                                                                                                                                                                                                                                                                                                                                          Center clone name: 427_K 12
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                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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1 (bases I to 155753)

Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone CTD-252514

Unpublished

2 (bases I to 155753)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastelien, V., Boguelarkiy, L., Boukhgalter, B., Anderson, S., Barran, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
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Homo sapiens chromosome 15, clone CTD-252514, complete sequence.
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95.0%; Pred. No. 44;
ive 0; Mismatches
                                                                                                12731. 12760

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13261. 13403

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complement (13906. 14971)

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family="(TTTA)n"
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family="(TA)n"
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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.

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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pietre, N., Hagos, B., Haaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McMeneus, E., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mcenan, Y., Murphy, T., Naylor, J., Nguyen, C., Orbunell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Kiley, R., Schauer, S., Schupback, R., Senach, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Travis, N., Subramanian, R., Zimmer, A. and Zody, M., Travis, M., Shore, J., Myman, D., Ye, W.J., Young, G., Direct Subnission, M., Laimer, A. and Zody, M., Travis, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shore, M., Shor
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Direct Submitsolon

Bubmitted (166-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 15573)

Sarna, N. Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Cheepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., PitzGerald, M., Gage, D., Galagan, J., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Macdonald, P., Major, J., Matchews, C., McCarthy, M., Maclean, C., Macdonald, P., Major, J., Matchews, C., McCarthy, M., Maddrim, J., Morye, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Scaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talawers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Traverer, M., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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AUTHORS

REFERENCE

REPERENCE

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Only the first 155.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC013489 [WICGR project
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1219. 1872
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complement(2541. .2615)
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complement(2628. .2770)
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Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Taegteye, S., Torruella-Miller I., Vassiliev, H., Vok.A., Magner, A., Taegteye, S., Torruella-Miller I., Vassiliev, H., Vok.A., Magner, A., Taegteye, S., Torruella-Miller I., Vassiliev, H., Vok.A., Magner, A., Miseal I. Ortralla-Miller I., Vassiliev, H., Vok.A., Magner, D., Malan, S., Dolage, S., Charler, S., Charler, B., Barnan, N., Bastlen, V., Bloom, T., Boggislavki, L., Boukgalter, B., Barnan, N., Bastlen, V., Bhoom, T., Boggislavki, L., Boukgalter, B., Gords, C., Chock, P., Dekar, D., Charler, B., Grand-Pierre, N., Hagos, B., Martan, M., Rells, C., Landers, P., Gard-Pierre, N., Hagos, B., Kartas, A., Kells, C., Hievine, R., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Lindhlad-Toh, K., Elsere, N., Hagos, B., Marthews, C., McChauer, S., Macol, R., Morbu, T., Matthews, C., Monnor, T., Wolly, P., Pierre, N., Raymond, C., Retze, R., Rise, C., Rooman, C., Sordhuer, S., Schuer, S., Schlauer, S., Schlauer, S., Schlauer, S., Schlauer, S., Schlauer, S., Schlauer, S., Theodore, J., Topham, K., Travers, M., Vasailiev, H., Visl, R., Jahmas, J., Teefeye, S., Theodore, J., Topham, K., Travers, M., Vasailiev, H., Visl, R., Jahmes, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, J., Jahmas, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24.AUG-2002) Whitehead Institute/MIT Center for Genome Submitted, 320 Charles Street, Cambridge, MA 02141, USA Con Aug 24, 2002 this sequence version replaced gi:22417381.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingron.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: 12244
Center clone name: 19_F_9
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Homo sapiens chromosome 18, clone RP11-19F9, complete sequence.
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Pred, No. 77;
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100.0%; Pre
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Homo sapiens chromosome 18 clone RP11-776M20 map 18q12, WORKING DRAFT SEQUENCE, 8 unordered pieces.
AP001356
AP01356.3 GI:9229949
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
Fel:81-42-778-9923, Fax:81-42-778-9924)
On Jul 15, 2000 this sequence version replaced gi:8117270.
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
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1 (bases 1 to 177456)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo saplens 177,456 genomic DNA of 18g12
Published Only in DataBase (2000)
2 (bases 1 to 177456)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Contact: hattori@gsc.riken.go.jp
------- project Information
Center project name: Humbrafil8
Center clone name: RP11-776M20
                                                                                                                                       /rpt_femily="(TGAA)n"
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28640. .28671
29132. .30007
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23473. ..23487
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complement(23513. .23779)
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27773. .27812
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34258. 34257
34258. 34523
34524. 36097
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36345. 36422
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AL928696 102448 bp DNA linear ROD 21-NOV-2002
Mouse DNA sequence from clone RP23-387G11 on chromosome 2, complete
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 102448)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2172)
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Submitted (11-JUN-1998) Physiology, University of Manitoba, 770
Bannatyne Ave., Winnipeg, MB R3E 0W3, Canada
Location/Qualifiers
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Isolation and characterization of the mouse beta 2/neuroD gene
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               Length 177456;
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Pred. No. 3e+02;
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2091. .>2172
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/note="helix-loop-helix protein"
                           DB 2;
76;
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                           90.0%; Score 18; DB ilarity 100.0%; Pred. No. 76; Conservative 0; Mismatches
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44898 77452 contig of 32555 bp in length
17553 105748 contig of 28196 bp in length
105849 132030 contig of 28196 bp in length
132131 145722 contig of 28592 bp in length
165329 172568 contig of 10406 bp in length
172469 172568 contig of 7040 bp in length
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Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator Er-amersham; 100% of reads Chemistry: Dye-terminator Er-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 174936 bases at least Q40 Consensus quality: 17605 bases at least Q30 Consensus quality: 176652 bases at least Q20 Insert size: 176756; sum-of-contigs Quality coverage: 11.10x in Q20 bases; sum-of-contigs
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1 44797: contig of 44797 bp in length
798 44897: gap of 100 bp
898 77452: contig of 32555 bp in length
453 77552: gap of 100 bp
553 105748: contig of 28196 bp in length
749 105848: gap of 100 bp
849 132030: contig of 26182 bp in length
849 132130: gap of 100 bp
131 154722: contig of 26182 bp in length
723 154822: gap of 100 bp
723 165228: contig of 100 bp
723 165228: contig of 100 bp
723 165228: contig of 100 bp
724 165328: gap of 100 bp
725 165228: contig of 100 bp
726 17268: gap of 100 bp
7276 17268: gap of 100 bp
726 17268: contig of 7040 bp in length
727 17268: gap of 100 bp
726 17468: gap of 100 bp
727 1746: contig of 4988 bp in length
728 17468: gap of 100 bp
729 17468: gap of 100 bp
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note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSERCT; Tr:, TERMBL; WP:, WORNPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-387G11 is from the RPCI-23 Mouse PAC Library deconstructed by the group of Pieter de Jong.

FOR further details see http://www.chori.org/bacpac/home.htm
                       Submitted (21-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 22, 2002 this sequence version replaced gi:25135705.
Sequence from the Mouse Genome Sequencing Consortium whole genome shocgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a prired quality of at least 30.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 140334)
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Homo sapiens, clone RP11-28C3, complete sequence.
ACO21802
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Unpublished
                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
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/clone="RP23-387G11"
/clone_lib="RPCI-23"
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Best Local Similarity 94.74
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                   Center code: SC
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Anderson, S., Baldwin, J., Barchard, S., Backerly, R., Beda, F., Bodulavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collinas, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dowle, M., Fenrestor, J., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, M., McEwan, P., McGurk, A., McKernan, K., McRentan, E., McGurk, A., McKernan, K., McRentan, E., Mollar, M., McBwan, P., McGurk, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Pierre, M., Fisani, C., Pollara, V., Raymond, C., Rilley, K., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Wol, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wiel, R., Wol, X., Wyman, D., Ye, W.J., Direct Submission
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(CB 3 (bases 1 to 140334)

(CB 3 (bases 1 to 140334)

(CB Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastelano, A., Campopiano, A., Chng, J., Chazaro, B., Cohagelo, M., Collymore, A., Cook, P., Codagelo, M., Collymore, A., Cook, P., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hadoos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McBwan, P., McGarran, K., McPheeters, R., Meldrim, J., McGarthy, M., McBwan, P., Marquis, T., Naylor, J., Naylor, J., Naphova, T., Manga, V., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Naylor, J., Schupback, R., Sahace, S., Schubback, R., Sewert, M., Roy, A., Santos, R., Schauer, S., Schubback, R., Sewert, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Yoblier, J., Nalson, B., Wilson, B., Wilson, B., Wilson, B., Willey, M., Triglillo, J., Vassiliev, H., Viel, R., Submitted, M., Travis, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Submitted, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Submitted, M., Subramanian, A., Andrich, A., Andrich, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Submitted, M., Subramanian, A., Andrich, A., Andrich, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Submitted, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Willey, M., Wan, Wann, M., Wan, Wann, Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., Wan, M., 
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All repeats were identified using RepeatMasker:
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------ Project Information
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Web site: http://www-seq.wi.mit.edu
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repeat\_region

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10619. 10737
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10997. 11136
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6820. 6953

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AC133524 GI:22830237
HTG; HTG; PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
SM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mus musculus
Eukaryota; Materaton, R.H.

Roberson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
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Mus musculus chromosome UNK clone RP23-43L4, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
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Best Local Similarity 94.7<sup>†</sup>
Matches 18; Conservative
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ACO26086 191426 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 15 clone RP11-540N15, WORKING DRAFT
SEQUENCE, 26 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:8568910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 100 sequencing vector: plasmid; 0% chemistry: Dye-primer ET; 100% creads chemistry: Dye-primer ET; 100% coresens chality: 18024 bases at least Q40 consensus quality: 18024 bases at least Q30 consensus quality: 185399 bases at least Q30 consensus quality: 185399 bases at least Q20 linsert size: 203000; agarose-fp insert size: 203000; agarose-fp Quality coverage: 4.00 in Q20 bases; agarose-fp Quality coverage: 4.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
Center code: WUGSC
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1854: gap of unknown length
4193: contig of 2339 bp in length
4193: gap of unknown length
6143: contig of 1850 bp in length
7809: contig of 1866 bp in length
7809: contig of 1866 bp in length
7809: contig of 1866 bp in length
7809: contig of 1849 bp in length
7858: contig of 1849 bp in length
15460: contig of 1849 bp in length
18198: contig of 2502 bp in length
18198: gap of unknown length
18198: gap of unknown length
2182: contig of 3584 bp in length
2182: contig of 3584 bp in length
2182: contig of 3584 bp in length
25547: contig of 3585 bp in length
25647: contig of 3885 bp in length
25647: contig of 3882 bp in length
2869: gap of unknown length
2869: gap of unknown length
28669: gap of unknown length
28669: gap of unknown length
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bp in length
length
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                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Homo sapiens clone Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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gap of u
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Waterston, R.H.
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Waterston, R.H.
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28569:
32543:
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39611:
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                                                   Submitted (14-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 04
Sequencing vector: plasmid; 1004
Chemistry: Dye-primer ET; 04 of reads
Chemistry: Dye-primer ET; 04 of reads
Chemistry: Dye-terminator Big Dye; 1004 of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 18736 bases at least Q30
Consenus quality: 187326 bases at least Q20
Insert size: BAC96; agarose-fp
Insert size: 190782; sum-of-contigs
Quality coverage: 12.95 in Q20 bases; sum-of-contigs
Quality coverage: 771 in Q20 bases; sum-of-contigs
                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                   1969: contig of 1969 bp in length 2069: gap of unknown length 5013: contig of 2944 bp in length 5113: gap of unknown length 11567: contig of 6454 bp in length 11667: gap of unknown length 60663: contig of 48996 bp in length 60763: gap of unknown length 60763: gap of unknown length 189983: contig of 129220 bp in length
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1.189983
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/chromosome="UNK"
                                                                                                                                      ----- Genome Center
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Best Local Similarity 94.7<sup>3</sup>
Matches 18, Conservative
                      Direct Submission
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48242: contig of 8531 bp in length 48242: contig of 8531 bp in length 54805: contig of 8643 bp in length 54805: contig of 6463 bp in length 62691: contig of 7786 bp in length 62291: gap of unknown length 7084: contig of 7786 bp in length 70884: gap of unknown length 70884: gap of unknown length 80151: contig of 9267 bp in length 80151: contig of 9267 bp in length 90121: gap of unknown length 90121: gap of unknown length 99341: contig of 9429 bp in length 12 14999: contig of 18458 bp in length 12 14999: contig of 18458 bp in length 12 14999: contig of 11302 bp in length 15099: gap of unknown length 15099: gap of unknown length 1500 129243: contig of 14144 bp in length 14645: contig of 17302 bp in length 16352: contig of 19095 bp in length 158 186452: gap of unknown length 158 186452: gap of unknown length 158 186452: gap of unknown length 16352: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16352: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16353: contig of 2408 bp in length 16354: contig of 2408 bp in length 16354: contig of 2408 bp in length 16354: contig of 2408 bp in length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of unknown length 16360: gap of un
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80252. .89912
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/note="assembly_name:Contig23"
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8299. .1882
"note="assembly_name:Contigl6"
11983. .25847
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/note="assembly_name:Contig24"
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note="aggembly_name:Contig14"
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8570. .32543
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL627104 193363 bp DNA linear ROD 15-NOV-2002
Mouse DNA sequence from clone RP23-412B2 on chromosome 4, complete
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Leongamornlert, D. Bottomia; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; Butheria; But
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cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
numquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
n Aug 11, 2002 this sequence version replaced gi:20793071.
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Tavers, M., Vasiliav, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

AL Submitted (12-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

A (bases 1 to 194546)

Research, 320 Charles Street, Cambridge, MA 02141, USA

A (bases 1 to 194546)

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chararo, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farcira, P., FitzGerald, M., Gage, D., Galagan, J., Garham, L., Grand, Pletre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Machen, C., MacGonald, P., Major, J., Maneus, L., Mihova, T., Mienga, V., MacJen, C., MacGonald, P., Major, J., Meneus, L., Mihova, T., Mienga, V., Phunkham, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkham, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkham, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vallen, R., Wyman, D., Young, G., Zainoun, J., Viel, R., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 1, 2002 this sequence version replaced gi:22381569. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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1. Diagonal Share, A. Chaese I to 194546)

Sarra, N., Backlein, V., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dewar, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Deverlano, K., Dewar, K., Diaz, J.S., Collymore, A., Goyette, M., Graham, L., Grand-Pierre, N., Gade, D., Galagan, J., Gardyns, S., Ginde, S., Gyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Hotron, L., Hulme, W., Iliev, I., Johnson, R., Lohocs, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lebrozky, J., Levine, R., Liu, G., Machan, C., Macchan, R., Marquis, N., Matthews, C., McZarth, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Marquis, N., Matthews, C., Nordu, C., Norman, C., Roter, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Stener, S., Schupback, R., Stohaver, S., Schupback, R., Stohaver, S., Schupback, R., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Stohaver, S., Tresfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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Homo sapiens chromosome 15, clone RP11-540N15, complete sequence.
ACO87482
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Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-540N15
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         VECTOR: pBACe3.6.
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us-09-899-276c-8.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MLT1L"
complement(17855..18179)
                                                                                                                                                                                                    /rpt_family="Alusx"
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0. .21279
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1848. .7934
                                                                                                                                                                                                                                                                                                                                                                                                  rpt family="LIMEd"
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9585.
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2090<u>1</u>.
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20804.
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1 (Dasses 1 to 208945)

KNIZNY, D.Maile., McAREY, M.Lee., Abramazon, S., Adams, C., Alder, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC125890 208945 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-281JJ7, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                             Gaps
                                                                                                                          Length 194546;
                                                                                                                                                                                             ;
0
                                                                                                                                                                                             Indels
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HTG, HTGS PHASE2, HTGS_DRAFT, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                          Score 17.4; DB 9;
Pred. No. 1.6e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                               2 GAAGGIIGAGICAAGGAIT 20
                                                                                                                                    Query Match 87.0%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                 repeat_region
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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AC125890
LOCUS
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AUTHORS
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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Monicular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23195060.

The sequence in this assembly is a combination of BAC based reads and whole genome shortun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, bidividual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence reads. Both end sequences and whole genome shortun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.
                                                                                                                                                                                                 Worley, K.C.
Direct Submission
Submitted (JuL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Ret Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: CH230-281J17
Assembly program: Phrap; version 0.990329
Consensus quality: 167086 bases at least Q40
Consensus quality: 177081 bases at least Q30
Consensus quality: 177471 bases at least Q30
Estimated insert size: 178699, sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
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clone_end:T7"
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/db_xref="taxon:10116"
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8551. .10700
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'note="clone_boundary
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10 (Dases I to 22485)

Muzny, D. Marte., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alabrooks, S., Amin, A., Anguiano, D., Allan, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiabechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Blankenburg, K., Blath, P., Brown, M., Blankenburg, K., Blath, P., Brown, M., Bryth, N., Blath, P., Brown, M., Bryth, N., Blath, C., Blankenburg, K., Calderon, E., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Chae, K., Chavez, D., Danson, S., Derawo, C., Diny, Y., Chal, T., Parda, C., Dedrich, D., Darger, H., Dugar-Rochas, D., Denson, S., Derawo, C., Diny, Y., Chal, T., Fan, G., Perandez, S., Filley, M., Eugene, C., Ryan, C.A., Garra, M., Gabrey, P., Fernandez, S., Filley, M., Eugene, C., Ryan, C.A., Garra, M., Gabregeorgie, E., Geer, K., Gilley, M., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, M., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Jacob, L., Jang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Lu, X., Man, M., Mahillos, M., Mahilloy, K., Martinez, E., Maveshwari, M., Mahindarine, M., Mahindarine, M., Mahindarine, M., Mahindarine, M., Mahiner, G., Mula, E., Morten, R., Morten, S., Parks, K., Martines, K., Martines, S., Parks, K., Martines, S., Parks, K., Martines, S., Parks, K., Martines, S., Parks, K., Marter, M., Man, M., Mortis, S., Munidas, M., Mulloy, R., Reigh, R., Pasternak, S., Paul, H., Perez, L., Pfannkoch, C., Reigh, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., R
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Rattus norvegicus clone CH230-7M13, WORKING DRAFT SEQUENCE.
AC095610
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.4; DB 2; Length 2
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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/note="wgs_contig"
207618. .208514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGAAGGTTGAGTCAAGGAT 19
                                                                                                                                                                                                                                                                                                                                             clone_end:Sp6
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Best Local Similarity 94.7%;
Matches 18; Conservative
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\mathtt{site}:\overline{\mathtt{E}}\mathtt{coR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley. K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

Stat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department

Direct Submission

Submitted (09-MAY-2003) Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:22772229.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgus sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence only contigs will be indicated in the feature

table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contiggs. Gaps between the contiggs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sterong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Wallson, D., Waldron, L., Walker, B., Wang, J., Wallson, R., Waldron, L., Walker, B., Wang, J., Williams, G., Willson, R., Wacker, R., Wooden, H., Worley, K., Wight, D., Wright, R., Wuly, Yakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, J., Yakub, S., Yen, J., Yoon, U., Weinstock, G. and Gibbs, R.A. Birth, D.R., Holt, R.A., Smith, H.O., Winstell Submission
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	c 50	15.8	79.0	1394	9	ADG90913	

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79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0
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## ALIGNMENTS

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. 88; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Poustka A; Human MCP-1 related oligonucleotide SEQ ID NO:8. Finzer P, Delius H, Disclosure; SEQ ID NO 8; 30pp; English. (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. ADH13945 standard; DNA; 20 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. EP1170372-A1. Homo sapiens 09-JAN-2002. ADH13945; ADH13945
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The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. or carcinoma. A atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.
                                                                                                                                                                                                                                       ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer;
                                                                                                                                                                                                Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:1.
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gene knockout; Cc12-deficient; Ccr2-deficient; drusen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delius H, Poustka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 600 BP; 213 A; 101 C; 150 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Cc12 gene and enhancer region DNA SeqID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 1; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finzer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.00,
100.0%; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD003803 standard; DNA; 11793 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GGAAGGTTGAGTCAAGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-2000; 2000EP-00114560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-2000; 2000EP-00114560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%;
                                                                                   ADH13938 standard; DNA; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGAAGGTTGAGTCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U, Coy J,
Patzelt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 17; Conservative
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-165895/22.
                                                                                                                                                                                                                                                                                            cervical carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roesl F, Soto
Zur Hausen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             EP1170372-A1
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                                                                                                                                                                    11-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                            ADH13938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO03803
                                           RESULT 3
ADH13938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *****
                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoatrractant-protein.1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human monocyte-chemoattractant-protein-1 AP-1 binding site SEQ ID NO:10.
pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poustka A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 6; Length 21;
Pred. No. 53;
                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                             Seguence 20 BP; 6 A; 1 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delius H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 10; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finzer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                            1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                    1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                        ADH13947 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soto U, Coy J,
H, Patzelt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zur Hausen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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09-JAN-2002

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11-MAR-2004

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Gaps

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Length 600; 0; Indels

DB 6; 80;

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Query Match

Matches

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II) and useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The colypeptide and polynuclectide sequences have applications in a produce other trypes of data and products dependent on DNA and and cand to produce other trypes of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1152 BP; 318 A; 286 C; 253 G; 295 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; DB 5; Length 1:
90.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 35028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 5539; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC42300 standard; DNA; 1604 BP
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99US-0123180P.
99US-0123548P.
                                                                             Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2000 (first entry)
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Matches 18, Conservative
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                                                                             Drmanac RT, Liu C,
                                                                                                                           WPI; 2001-639362/73
                            (HYSE-) HYSEQ INC
                                                                                                                                                     P-PSDB; ABG05548
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05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, CCr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or repression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions whilbit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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membrane; retinal degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 17; DB 12; Length 11793;
Pred. No. 1.2e+02;
Mismatches 0; Indels 0
                         choroidal neovascularisation; ophthalmological; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #5539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 17; DB 100.0%; Pred. No. 1.2 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4; 64pp; English.
  lipofuscin accumulation; Bruch's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS69735 standard; cDNA; 1152 BP
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                                                                                                                                                                                                                      16-OCT-2003; 2003WO-US032933.
                                                                                                                                                                                                                                                                       30-OCT-2002; 2002US-0422096P.
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 100.0
....hes 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accumulation in eye.
                                                                                                                    WO2004041160-A2
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                                                                                                                                                                                                                                                                                                                                                                      Ambati J;
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RESULT 5 AAS69735/c

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New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
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990S-0160761P.
990S-0160761P.
990S-0160814P.
990S-0160814P.
990S-0160814P.
990S-0160815P.
990S-0160815P.
990S-016180P.
990S-016185P.
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                                                                                                                                                                                                                                                                                                                                                                                        1989/c
ADQ97989 standard; DNA; 59002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2002; 2002US-00330773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                            84.0%;
                                                                                                                                                                                                                                                                                       90.06;
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malandro MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-543781/52.
                                                                                                                                                                                                                                                                                       Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004060304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
 14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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22-0CT-1999;
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28-0CT-1999;
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Matches
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94.48;

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Best Local Similarity 94.4
Matches 17; Conservative
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Fragment Name
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ADQ97050_3
ADQ97050_3
ADQ97050_4
ADQ97050_5
ADQ97050_5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                             ADQ97050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS20588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
AAS20588/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or T has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention. N.B. Polymorphic bases (single nucleotide polymorphisms also known as SNPs) in the polymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; dentification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
                                                      Sequence 59002 BP; 16030 A; 11777 C; 12009 G; 18102 T; 0 U; 1084 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism.
                                                                                                                                                                   Gaps
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                                                                                                            Length 59002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 939 BP; 249 A; 187 C; 246 G; 256 T; 0 U; 1 Other;
                                                                                                                                                                Indels
                                                                                                          Score 16.8; DB 12;
                                                                                                                                 Pred. No. 1.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chumakov I;
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 693; 802pp; English.
                                                                                                                                                                                                                                                                          7393 GGAAGGATGAGTCAAGCATT 7374
                                                                                                                                                                                                                    1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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99US-00275267.
99US-0133200P.
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                                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-1999;
23-MAR-1999;
07-MAY-1999;
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82.0%; Score 16.4; DB 3; Length 939;

Query Match

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ADQ97050 from base 500001 (Human cancer associated sequence HD: fragments LOCUS ADQ97050 Accession Adq97050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; methionine aminopeptidase; protease; adrenal cortico adenoma; ds;
Cushing's syndrome; prostate embryonal carcinoma; colon tumour; brain;
hepatocellular carcinoma; foetal lung; testis; b cell; kidney; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule encoding methionine aminopeptidase, useful for the development of human therapeutics and diagnostic compositions.
                              Gaps
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Pred. No. 1.8e+02;
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Pred. No. 3.2e+02;
); Mismatches 1;
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310000
410000
510000
610000
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                                                                                        548 GGAAGGTTGAGTCAAGCA 565
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300001
400001
500001
600001
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Continuation (6 of 7)
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AAL11857 standard; cDNA; 433 BP
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15-MAY-2000; 2
09-JUN-2000; 2
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24-MAR-2000;
                                                                                                                                               Ношо заріепв
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                                                     AAL11857;
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Matches
         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
hepatocellular carcinoma, foetal lung, testis and b cell, kidney
                                           Seguence 84495 BP; 23805 A; 16441 C; 17154 G; 25835 T; 0 U; 1260 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
          and prostate. This sequence represents genomic DNA encoding the human methionine aminopeptidase of the invention
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide useful as a marker for the diagnosis of breast cancer.
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                                                                 80.0%; Score 16; DB 6; Length 84495;
100.0%; Pred. No. 5e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 399 BP; 123 A; 55 C; 132 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              Human breast cancer expressed polynucleotide 13204
                                                                                                                                                                                                                                                                                     Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinmann K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2342; 3695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GAAGGTGGAGTCAAGAATT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGGITGAGICAAGGAIT 20
                                                                Query Match
Best Local Similarity 100.0%; Pr.
Matches 16; Conservative 0;
                                                                                                                                        34427 GGAAGGTTGAGTCAAG 34412
                                                                                                                                                                                               AAL20747 standard; cDNA; 399 BP
                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0176077P.
2000US-0189167P.
2000US-0192099P.
2000US-0193480P.
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                                                                                                                 1 GGAAGGTTGAGTCAAG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity
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14-MAR-2000; 2
24-MAR-2000; 2
29-MAR-2000; 2
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The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polynethially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                 Human breast cancer expressed polynucleotide 4314.
                                                                                    88.
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Pred. No. 3.3e+02;
0; Mismatches 2;
                                                                                  Human; breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast cancer related marker, seq id 3203.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 783; 3695pp; English.
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; 2000US-0189167P.
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; 2000US-021315P.
; 2000US-0210315P.
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20-OCT-2000; 2000US-0240960P.
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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 ö
                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent mucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
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                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 3203; 36pp; English
                                                                                                                                                                    Lillie J, Xu Y, Wang Y, Steinmann K;
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2000US-018062BP.
2000US-018464P.
2000US-0189374P.
2000US-0199074P.
2000US-01990176P.
                                                                         18-JUL-2002; 2002US-00198846
                                                                                                     18-JUL-2001; 2001US-0306220P
                                                                                                                                    (MILL-) MILLENNIUM PHARM INC
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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Matches
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17-NOV-2000; 2000US-0249264F.
17-NOV-2000; 2000US-0249264F.
17-NOV-2000; 2000US-0249265F.
17-NOV-2000; 2000US-024929F.
17-NOV-2000; 2000US-0249300F.
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05-DEC-2000; 2000US-025198F.
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20-0CT-2000; 2
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20-0CT-2000; 2
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Rosen CA, Barash SC, Ruben SM WPI; 2001-483426/52. P-PSDB; AAM83415.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 1; SEQ ID NO 1256; 3071pp + Sequence Listing; English.

AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and

ö treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to press the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of hemantopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54550 and AAM32169 represent sequences used in the exemplification of the present invention Gaps ö Query Match 79.0%; Score 15.8; DB 4; Length 462; Best Local Similarity 89.5%; Pred: No. 3.38+02; Matches 17; Conservative 0; Mismatches 2; Indels C Seguence 462 BP; 96 A; 134 C; 137 G; 91 T; 0 U; 4 Other; 1 GGAAGGTTGAGTCAAGGAT 19 183 g ઠ

4, 2005, 08:31:32 Search completed: August Job time: 16.2551 secs

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AZ795398 2M0049B10
AZ100790 EST2210069
AG180768 Pan trog1
AG88174 HZ 3153 B
CC836847 ZWEBEC048
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CG558504 GST434651
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CG463871 tigr-gss-
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                                                        OM nucleic - nucleic search, using sw model
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BZ820561 PUGBH74TD AQ29288 H 82231 A BQ29288 H 82231 A BU291070 604164287 AZ032655 RPCI-23-3 BQ403091 GA_Ed005 BG44258 GG_Ed005 BW319959 BW119959 BW319959 BW119959 BW319959 BW319959 BW31955 BW119959 BW31955 BW119959 BW31955 BW119959 BW31955 BW119959 BW31955 BW119959 BW31955 BW119959 BW31959 BW317210	ALIGNMENTS  AJ516664  AJ516664  AJ516664  Mytilus galloprovincialis haemolymph, gills, digestive gland, foot, adductor muscles and mantle Mytilus galloprovincialis and mantle Mytilus galloprovincialis aductor muscles and mantle Mytilus galloprovincialis (Mediterranean mussel)  Mytilus galloprovincialis (Mediterranean mussel)  Mytilus galloprovincialis (Mediterranean mussel)  Mytilus galloprovincialis (Mediterranean mussel)  Mytilus galloprovincialis  Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;  Mytilus galloprovincialis  Towards a catalogue of genes transcribed in multiple tissues of Mytilus galloprovincialis  22890058  14527715  Contact: Venier P  Enodosy  University of Padova  Via Ugo Bassi 58/b, Italy, 34100, Italy.  Location/Qualifiers  1. 400    Acronism="Mytilus galloprovincialis"     Abology    Abology   Moly xref="taxon:29158"     Clone="Expression" (1918)   Abology     Abolo	1; Length 3e+02; 0; Ind
BZ820561 BP259697 BQ2290288 BQ2290288 BQ2200091 BG442583 BW119959 BW119959 AW037663 CN45627 BW37210 BQ587296 BQ41630 CD823901 CD823901 CD823901 CD823901	ALIGNMENTS  AJ51664 AJ51664 Mytilus galloprovincialis haemolym gland, foot, adductor muscles and mantle My cDNA clone GPPD00678, mRNA sequence. AJ51664.1 GI:37650241 ENTILUS galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Mediterranean mu Mytilus galloprovincialis (Gases Ito 400)  TOWARCA: Metazoa; Mollusca; Bivalvia; Pte Mytilus galloprovincialis (Gases Ito 400)  TOWARCA: Pallavicini, A., De Nardi, B. and TOWARCA: A Catalogue of genes transcribed in Mytilus galloprovincialisology  University of Padova  Location/Qualifiers  L. 400  / organism="Mytilus galloprovincial/" (Clone="GPPDD0679")  / clone="GPPDD0679"  / tissue="Type="MRNA"  / clone="GPPDD0679"  / clone="GPPD06679"  / clone="GPPD06679"  / clone="Lib="Mytilus galloprovincial/" (Clone="GPPD0679")  / clone=  lib="Mytilus galloprovincial/" (Clone="Lib="Mytilus galloprovincial/")  / clone=  lib="Mytilus galloprovincial/" (Clone="Lib="Mytilus galloprovincial/")	Score 18; DB; Pred. No. 3. 0; Mismatches 20
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<ul> <li></li></ul>	AJ51664 My J51664 My J51664 My Jand, foot CDNA clone AJ51664 LBST.  Mytilus gal Mytilus ga	imilarit ; Conse AAGGTTGP AAGGTTGP
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000 00 0 000	RESULT AJ51666 LOCUS DEFINIT ACCESSI VERSION KEYWORD SOURCE ORGAN TITLE TITLE TITLE PUBM COMMENT	ORIGIN Quer Best Matc Qy Db

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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 361)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
Direct Submitted (12.2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
CR008527

Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN202111, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ785398 16-FEB-200
2M0049B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0049B10 R, genomic survey sequence.
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Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels (
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Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                              CR008527
CR008527.1 GI:49741518
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus

    .453
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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/clone="MHPN202111"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynanically sheared by repeated passage through a was hydrodynanically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalpq2 (gil 4732114 gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                  /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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1 (Dases 1 to 580)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Jundax
Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-0208
Email: nhlee@igr.org
Seq primer: M13-21.
Seq primer: M13-21.
Seq primer: M3-21.
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0; Mismatches 1; Indels (
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/mol_type="mRNA"
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/clone="RBRBA18"
                                                                                                                                                                                                        Laboratory Mouse DNA Resource
'db_xref="taxon:10090"
                         clone="UUGC2M0049B10"
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Email: bharti@waksman.rutgers.edu
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94.7%;
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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-40G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@scritken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ898174 832 bp DNA linear GSS 10-NOV-1999 HS 3153 B1 C07 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3153 Col=13 Row=F, genomic survey sequence.
AQ898174 GI:6354364
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: RP43-053H03.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                           Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
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 87.0%; Score 17.4; DB 1; Length 580; 94.7%; Pred. No. 7e+02; 1:ve 0; Mismatches 1; Indels
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/organism="Pan troglodytes"
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Pan troglodytes
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AG180768.1 GI:16710448
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                                 18; Conservative
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Matches 18; Conserv
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   Query Match
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SM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

I (bases 1 to 284)

S Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.

Sequencing of the maize genome at PGIR (2003b)

L Unpublished (2003)

Contact: Bharti,A.K.

Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 832)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Mahairas, G.G., Mallace, T., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZMWBBC0482F11r ZMWBBc Zea mays genomic clone ZMMBBc0482F11 3', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Blate: 3153 row: F column: 13
Seg primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CIT_Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=3153 Col=13 Row=F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 8;
Pred. No. 7.3e+02;
0; Mismatches 1;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
Contact: Pobert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ380590 537 bp DNA linear GSS 02-OCT-2000 1M0136P01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0136P01 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 537)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                      /organism="Zea mays"
/mol type="genomic DNA"
/cultivar="H37"
/clone="zawhBBc482F11"
/lab_host="E. coli DH10B"
/clone lih="zawhBBc"
/note="Vector: pTARBAC1.3; Site_1: BamH1; Site_2: BamH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain Xil0-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0136 row. P column: 01
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC1M0136P01"
Seg primer: SP6
Class: BAC ends
High quality sequence start: 97.
Location/Qualifiers
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AZ380590.1 GI:10494290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 308, Bi
84112, USA
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAPA2 (gil JA72114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 771)

SNIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

LUpublished (1999)

LUpublished (1999)

LUpublished (1999)

LOOMACE: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Email: cgapbs-radioni: Michael J. Brownstein (NHGRI), Shiraki cDNA Library Preparation: Michael J. Brownstein (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 708.

High quality sequence stop: 708.

Location/Qualifiers
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Homo sapiens
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DEFINITION

CC558114

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ORGANISM

REFERENCE

VERSION KEYWORDS SOURCE ACCESSION

TITLE JOURNAL COMMENT

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308 bp mRNA linear EST 11-AUG-2004
AJ792516 Antirrhinum majus whole plant Antirrhinum majus CDNA clone
AJ792516
                                                            CC675901 305 bp DNA linear GSS 19-JUN-2003
OGWEH38TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0558H04,
                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
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Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z. Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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Mittelaw, C. R., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, R.W., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSS: OGWEH38TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4577"
/clone="zwmBwa0558H04"
/clone=lib="zm_0.7 1.5_KB"
/note="wcctor: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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9712 Medical Center Drive, Rockville, MD 20850, USA
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels

    .308
    /organism="Antirrhinum majus"

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/strain="B73"
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90.0%; Pred
0; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                  genomic survey sequence.
CC675901
CC675901.1 GI:32080599
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/organism="Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
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Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
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Zea mays
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SOURCE
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AJ792516
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                                                                                                                                                                                                                                                                                        CH240 466N17.T7 CHORI-240 Bos taurus genomic clone CH240_466N17, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson J. (Dases 1 to 281)
Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Halt,R., Cloutier,A., Lee,D., Girn,M., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Other GSSs: CH200 466N17.TARBAC13P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
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84.0%; Score 16.8; DB 9; Length 281;

Best Local Similarity 90.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels
                                                         Indels
Pred. No. 1.2e+03;
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_466N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Bos taurus"
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                                                                                                                                                   698 AAGGTTGAGTCAAGGAT 682
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                           100.0%;
                                                                                                                  3 AAGGTTGAGTCAAGGAT
                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (cow)
Bos taurus
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                           Best Local Similarity
Matches 17; Conserv
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source

FEATURES

RESULT 11

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ORIGIN

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Gaps

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PUBMED
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1 (Bases I to 315)

1 (Bases I to 315)

1 (Bases I to 315)

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1 (Bases I to 315)

1 (Bases I to any Cambridgeshire, CB10 15A, UK. B-mail enquiries: Campus, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: This sequence was generated from the T7 end of BAC 125C2. 125C2 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: Keygene. Further details: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY663202 RIKEN full-length enriched, 14.5 days embryo RP+/+ Rathke's pouches Mus musculus cDNA clone K720019C17 3', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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BX160484
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                                                                                                                                             Length 308;
/mol_type="mRNA"
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/db_xref="taxon:4151"
/db_xref="018_21_n02"
/tisoue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                             Score 16.8; DB 1;
Pred. No. 1.3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKEY-125C2"
/tissue type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                   335 bp
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                                                                                                                                                                                                                                                                              134 GGAAGGTTTAGTCACGGATT 153
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                                                                                                                                                                                                                                 1 GGAAGGITGAGICAAGGAIT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danio rerio (zebrafish)
                                                                                                                                                  Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity 90.0°
Matches 18; Conservative
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Riyosawa, H., Yagi, K.; Tomarui, Y., Ailasegawa, Y., (Acosani, A.)

Riyosawa, H., Yagi, K.; Tomarui, Y., Biake, J. M., Bratt, D., Buit, C.,

Robenbach, C., Cardenin, L.B., Caster, B. B., Bratt, D., Brusic, V.,

Bacinor, S., Beisel, W. M., Biake, J. M., Bratt, D., Brusic, V.,

Garibodi, M., Ossai, C., Codzik, A., Gaster, Bard, D., Bratt, D., Brusic, V.,

Garibodi, M., Ossai, C., Codzik, A., Gough, J., Cammond, S., Rayani, M.,

Rawaji, M., Assai, C., Godzik, A., Gugh, J., Cammond, S., Rayani, M.,

Rawaji, M., Assai, C., Godzik, A., Gugh, J., Cammond, S., Majcher, D.R.,

Munate, K., Oddo, T., Farani, M. J., Pate, G., J., Bamchandran, S.,

Ravai, T., Rohenback, T., Patenda, B., Satou, M., Shimeda, K.,

Sandali, M., Schow, K., Shirzaki, T., Wand, J., Ramachadran, S.,

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Unpublished (1997)
Other ESR3: u022C12.y1
Contact: Robert Straubberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL):
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                            AW321997

UO22C12.xl NCI_CGAP_Mam6 Mus musculus CDNA clone IMAGE:2609878 3'
Similar to gb:M38337 Mouse milk fat globule membrane protein E8
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/dev_stage="14.5 days embryo RP+/+"
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RP+/+ Rathke's pouches"
                                                                                                                                     Gaps
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                                                                                            Query Match

84.0%; Score 16.8; DB 6; Length 345;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                               mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40UP from Gibco
High quality sequence stop: 223.
Location/Qualifiers
                                                                                                                                                                                             154 GGAAGGTTGAGTCAGAGATT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                         1 GGAAGGTTGAGTCAAGGATT 20
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Matches 18; Conserv
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
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307 GGCAGGTTGATTCAAGGATT 288

Search completed: August 4, 2005, 14:32:52 Job time: 102.397 secs

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us-09-899-276c-8.rni

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August 4, 2005, 07:01:49; Search time 4.12146 Seconds (without alignments) 7940.282 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                         1 ggaaggttgagtcaaggatt 20
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Maximum DB seq length: 2000000000
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Sequence 12174, A Sequence 15535, A Sequence 1552, App Sequence 552, App Sequence 12505, A Sequence 16549, A Sequence 16549, A Sequence 15821, A Sequence 15821, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13525, A Sequence 13528, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13538, A Sequence 13
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Sequence 5, Appli
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Sequence 4, Appl
                                                      US-09-621-976-17595

US-09-641-638-552

US-09-949-016-12505

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US-09-949-016-12509

US-09-949-016-12509

US-09-949-016-15891

US-09-949-016-15891

US-09-949-016-15094

US-09-949-016-1265

US-09-949-016-1275

US-09-949-016-1275

US-09-949-016-1275

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-09-949-016-136383
-09-134-000C-466
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US-09-375-248-5
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Sequence 5415, Ap Sequence 51, Appl Sequence 1, Appli	133		Sequence 11692, A Sequence 12655, A Sequence 15572, A Sequence 16847, A	Sequence 15440, A Sequence 16320, A Sequence 12537, A
US-09-949-016-5415 US-08-858-207A-51 US-08-915-795-1	US-09-29-27-27-1 US-09-949-016-13589 US-08-961-527-87 US-09-949-016-13318	US-09-949-016-12/38 US-09-949-016-13652 US-09-949-016-17157 US-09-146-053-5	US-09-949-016-11892 US-09-949-016-12655 US-09-949-016-15572 US-09-949-016-16847	US-09-949-016-15440 US-09-949-016-16320 US-09-949-016-12537
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## ALIGNMENTS

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US-VJ-49-ULD-LIA14/C
; Sequence 12174, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   FILE REPERENCE: CL001307
   CURRENT APPLICATION NUMBER: US/09/949,016
   CURRENT FILING DATE: 2000-04-14
   PRIOR PLLING DATE: 2000-10-20
   PRIOR FILING DATE: 2000-10-03
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 2007012
   SOFTWARE FEATSEQ for Windows Version 4.0
   SEQ ID NO 12174
   LENDER HOLES TOWN NUMBER: 07231,498
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTWARE FEATSEQ for Windows Version 4.0
   SEQ ID NO 12174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15635, Application US/09949016
Patent No. 6812339
GERERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TILE REPERENCE: CLO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117870 GGAATGTTGAGTCAAGGTTT 117851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(153642); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-12174
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Best Local Similarity 90.v.
Best Local 18; Conservative
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US-09-949-016-15635/c
US-09-949-016-12174/c
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ORGANISM: Human
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NAME/KEY: allele
LOCATION: 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1755, Application US/09621976

patent No. 6639063

geneRAL INPORMATION:
APPLICANT: Unas Milne Edwards, J.B.
APPLICANT: Jobert, S.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICANTON: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17595

LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 16.4; D 94.4%; Pred. No. 98; Live 0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTESEQ for Windows Version 4.0
SEQ ID NO 15635
LENGTH: 153643
                                                                                                                                                                                                                                                                                                                                              117870 GGAATGTTGAGTCAAGGTTT 117851
                                                                                                                                                                                ; NAME/KEY: misc_feature
; LCCATION: (1)...(153643)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15635
                                                                                                                                                                                                                                                                                                                            1 GGAAGGITGAGICAAGGAIT 20
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.04
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-621-976-17595
                                                                                                                                         TYPE: DNA
ORGANISM: Human
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US-09-641-638-552
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RESULT 5

USA-10-170-097-552

Sequence 552, Application US/10170097

Sequence 552, Application US/10170097

Sequence 100. 6794143

Sequence 100. 6794143

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Gonen, Annick

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILER REFERENCE: GEN-TILAK2D1

CURRENT APPLICATION NUMBER: US 09/641,638

PRIOR FILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

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PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

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PRIOR PILING DATE: 1999-03-13
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JOCATION: 439

OCHER INFORMATION: 12-65-98: polymorphic base C or T
NAME/KEY: misc_binding

LOCATION: 419.-438

OTHER INFORMATION: 12-65-98.misl, potential

OTHER INFORMATION: 12-65-98.misl, potential

NAME/KEY: misc_binding

LOCATION: 440..459

OTHER INFORMATION: 12-65-98.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 342..360

OTHER INFORMATION: upstream amplification primer

NAME/KEY: misc_bind

LOCATION: 777..79

OTHER INFORMATION: downstream amplification primer, complement

LOCATION: 427..451

OTHER INFORMATION: 12-65-98 potential probe

US-09-641-638-552
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82.0%; Score 16.4; DB 3; Length 939;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels C
   PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 552
LENGTH: 939
APPLICATION NUMBER: US 09/275,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 GGAAGGTTGAGTCAAGCA 565
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                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
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GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: UGES THEREOF
FILE REPREMENCE: CLOOLISICEP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                      APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-3

PRIOR PLING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION VENER: 60/231,498

PRIOR APPLICATION VENER: 60/231,498

PRIOR APPLICATION VENER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

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Pred. No. 2e+02;
0; Mismatches 1; Indels 0;
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Pred. No. 2.6e+02;
0; Mismatches 0; Indels
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US-09-949-016-16549
Sequence 16549, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)....(670690)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14207
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LOCATION: (1)...(84495)
CTHER INFORMATION: n = A,T,C or G
US-09-797-906-3
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Best Local Similarity 100.0%; Powatches 16; Conservative 0;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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ORGANISM: Human
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SEQ ID NO 3
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEAGE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-9
PRIOR FILING DATE: 2000-10-9
PRIOR PILING DATE: 2000-10-9
PRIOR FILING DATE: 2000-10-9
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Pred. No. 2e+02;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                           LOCATION: 440.7459
OTHER INFORMATION: 12-65-98.mis2, potential complement
PEATURE:
OTHER INFORMATION: 12-65-98 : polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
                                                                          NAME/KEY: misc_binding
LOCATION: 419.7438
OTHER INFORMATION: 12-65-98.mis1, potential
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COTHER INFORMATION: 12-65-98 potential probe US-10-170-097-552
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 12505, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12505
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_binding
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US-09-949-016-14207
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LENGTH: 670689
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15821
LENGTH: 50563
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; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
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Best Local Similarity 89.5*
Matches 17; Conservative
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CRGANISM: Human
US-09-949-016-15821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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US-10-160-187-3/c
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US-09-741-150-3/c
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| Sequence 1258, Application US/09949016
| Patent NO. 6812339
| CENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOOL 307
| CURRENT FILING DATE: 2000-04-14 | 755 | PRIOR PLLING DATE: 2000-04-10-20 | PRIOR PLLING DATE: 2000-10-20 | PRIOR FILING DATE: 2000-10-03 | PRIOR FILING DATE: 2000-10-03 | PRIOR FILING DATE: 2000-09-08 | NUMBER OF SEQ ID NOS: 207012 | SEQ ID NO 12598 | LENGTH: 49673 | LENGTH: 49673 | LENGTH: 49673 | LENGTH: 49673 | LENGTH: 49673 | LENGTH: AP9673 | LENGTH: 49673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673 | LENGTH: AP9673
                                               APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16549

LENGTH: 47555
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Sequence 1581, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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... 2; Indels
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Pred. No. 3.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33158 GAAGGTTGAGTCATGGAAT 33176
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Best Local Similarity 89.57
Local 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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CRGANISM: Human
US-09-949-016-12598
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US-09-949-016-15821
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US-09-949-016-16549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Sequence 3, Application US/10160187
; Sequence 3, Application US/10160187
; Sequence 3, Application US/10160187
; Sequence 3, Application US/10160187
; GENERAL INFORMATION:
    APPLICANT: GUGGLER: Karl et al.
    APPLICANT: GUGGLER: SOLATED HUMAN PROTEASE PROTEINS,
    TITLE OF INVENTION: USES THEREOF
    FILLE REFERENCE: CL000968DIV
    FILLE REFERENCE: CL000968DIV
    CURRENT APPLICATION NUMBER: US/10/160,187
    CURRENT PILING DATE: 2002-06-04
    PRIOR APPLICATION NUMBER: 60/252,410
    PRIOR FILING DATE: 2000-11-22
    PRIOR FILING DATE: 2000-11-22
; PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS,
ENCODING HUMAN PROTEASE PROTEINS, AND
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Score 15.8; DB 4; Length 50563; Pred. No. 3.1e+02;
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                                                                       Indels
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Pst Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09741150

Patent No. 643669

GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PRO
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION UNMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTHAL 112132
                                                                    0; Mismatches
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15094
LESSEE OF WINDOWS VERSION 4.0
SEQ ID NO 15094
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                               Query Match 79.0%; Score 15.8; DB 4; Length 112132; Best Local Similarity 89.5%; Pred. No. 3.46+02; Matches 17; Conservative 0; Mismatches 2; Indels 0;
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79.0%; Score 15.8; DB 4; Length 209210;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 112132
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                                                                                                                                                                                                                                                                                                                                                                                                                         32191 GAAAGTTGAGACAAGGATT 32173
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                                                                                                                                                            NAME/KEY: misc_feature; CCATION: (1)...(112132); CTHER INFORMATION: n = A,T,C or G
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-949-016-15094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-949-016-12465
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                                                                                             TYPE: DNA
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August 4, 2005, 08:04:16; Search time 35.6761 Seconds (without alignments) 3633.986 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7297361 seqs, 3241162794 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM nucleic - nucleic search, using sw model
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 8, Appli Sequence 10, Appli Sequence 4, Appli Sequence 816, Appl Sequence 816, Appl Sequence 16253, A
SUMMARIES ID	9 US-09-899-276-8 9 US-09-899-276-10 9 US-09-899-276-1 19 US-10-685-705-4 21 US-10-950-009-816 19 US-10-950-009-816 17 US-10-170-097-552
DB	
% Query Match Length DB ID	20 21 600 11793 472 1817 939
* Ouery Match	100.0 85.0 85.0 84.0 84.0
Score	20 17 17 16.8 16.8
Result No.	ი 1004006

100.0%; Score 20; DB 9; Length 20;

Query Match

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US-10-926-684-552	-10-741-601-33	-10-741-600-	-10-741-600-31	-10-424-599-	0-425-115-	-10-425-115-8448	-10-027-63	-10-027-632-3671	-10-19	-10 - 42	-10-02	-10-02	-10-02	-10-027-63	-10-02	-10-02	5-11	US-10-424-599-134677	-10-198-84	-10-425-11	-10-424-599-5345	-10-425-11	US-10-739-930-3532	ķ	-437-963-5690	10-481-58	US-09-997-722-250	1-28	4	US-10-612-012-3	US-10-741-601-5641	US-10-741-600-17642	2	10-741-600-175	-10-317-883A-1	US-09-844-653-5
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939	207	201	201	366	367	394	427	427	459	477	507	507	507	507	570	570	617	648	758	820	1281	1385	2133	2595	4251	6675	96587	97415	112132	112132	112486	112486	161700	17	312477	402850
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## ALIGNMENTS

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US-09-899-276-8

US-09-899-276-8

Sequence 8, Application US/09899276

Patent No. US20020106355A1

GENERAL INFORMATION:

APPLICANT: Socto, Ubaldo

APPLICANT: Socto, Ubaldo

APPLICANT: Coy, Johannes

APPLICANT: Poustka, Annemarie

APPLICANT: Poustka, Annemarie

APPLICANT: Poustka, Annemarie

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APPLICANT: Poustka, Annemarie

APPLICANT: Poustka, Annemarie

APPLICANT: Poustka, Annemarie

APPLICANT: PARIENT POUSTOR: 012627-023

CURRENT FILING DATE: 2000-07-06

NUMBER OF SEQ ID NOS: 12

SOCTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

CHERRY PRINCEMATION: Part of 3'-DHSR

US-09-899-276-8
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APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Methods And Animal Model For Analyzing Age-Related Macular
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
TITLE OF INVENTION: Degeneration
FILE REPERBNCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT FILING DATE: 2003-10-16
RIOR FILING DATE: 2002-10-30
RIOR PILING DATE: 2002-10-30
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                            Gaps
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APPLICANT: BASHKIROVA, Elena
APPLICANT: BASHKIROVA, Elena
APPLICANT: REY, Michael
ITILIANT: REY, Michael
ITILIANT: REY, Michael
ITILIANT: REY, Michael
ITILIANT: REPERENCE: 10541.200-US
CURRENT APPLICATION NUMBER: US/10/950,009
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: 60/506,140
PRIOR PILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1190
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 816
Query Match 85.0%; Score 17; DB 9; Length 600; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 GGATGGTTGAGTCAAGGTTT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10136 GGAAGGTTGAGTCAAGG 10152
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10685705
Publication No. US20040177387A1
GENERAL INFORMATION:
                                                                                                                 1 GGAAGGTTGAGTCAAGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Trichoderma reesei
US-10-950-009-816
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Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-437-963-16253
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APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Finzer, Patrick
APPLICANT: Finzer, Patrick
APPLICANT: Poustka, Annemarie
APPLICANT: 2ur Hausen, Harald
APPLICANT: Pur Hausen, Harald
APPLICANT: Pur Hausen, Harald
APPLICANT: Pur Hausen, Harald
APPLICANT: Poustka, No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: NO. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
FILE REFERENCE: 012627-023
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT APPLICATION NUMBER: BO 00 114 560.6
FRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FasteSEQ for Windows Version 4.0
SEQ ID NO
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosl, Frank
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Gov, Johando
APPLICANT: Coy, Johando
APPLICANT: Coy, Johandaric
APPLICANT: Parzer, Parzick
APPLICANT: Delius, Hajo
APPLICANT: Dustka, Annemarie
APPLICANT: Lar Hausen, Harald
APPLICANT: Parzelt, Andrearie
APPLICANT: Parzelt, Andrearie
APPLICANT: Parzelt, No. US20020106355A1e1 Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: NO. US20020106355A1e1 Regulatory Sequences of the MCP-1 Gene
FILE REFERENCE: 012627-023
CURRENT APPLICATION NUMBER: EP 00 114 560.6
FRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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                                                 0; Indels
                        Pred. No. 2.7;
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                        Best Local Similarity 100.0%; Pred. No. 2.7
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-899-276-10
                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09899276 Patent No. US20020106355A1 GENERAL INFORMATION:
                                                                                                   1 GGAAGGTTGAGTCAAGGATT 20
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CRGANISM: Homo sapiens
US-09-899-276-1
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US-09-899-276-10
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US-10-926-684-55.

Sequence 52, Application US/10926684

Publication No. US20050014190A1

SEGNERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguelaret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: CARRYING
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID
FRIOR FILING DATE: 2002-06-10
FRIOR FILING DATE: 2000-08-16
FRIOR PELING DATE: 2000-08-16
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
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FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-03-13
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                                                                                                                                                                                                                                            NAME/KEY: primer bind LOCATION: 777..757 OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                            INFORMATION: 12-65-98.mis2, potential complement
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LOCATION: 440._459
OTHER INFORMATION: 12-65-98.mis2, potential complement
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 439
OTHER INFORMATION: 12-65-98 : polymorphic base C or T
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 17;
Pred. No. 2.7e+02;
                                                                                                                      NAME/KEY: primer_bind
LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_binding
; LOCATION: 427..451
; OTHER INFORMATION: 12-65-98 potential probe
US-10-170-097-552
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LOCATION: 419..438
OCHER INFORMATION: 12-65-98.misl, potential
FEATURE:
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Best Local Similarity 94.4%; Pri
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
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                                                                         APPLICANT: LA KOVALION:
APPLICANT: LA KOVALIC, David K.
APPLICANT: La Lou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wai wai
APPLICANT: Boukharov, Andrey A.
APPLICANT: Broukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
KUNBER OF SEQ ID NOS: 204966
SEQ ID NO 16253
LENGTH: 1817
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Publication No. US20030228582A1

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Annick

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GEN-T114XC2D1

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GEN-T114XC2D1

CURRENT APPLICATION NUMBER: US 09/641,638

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SEQ ID NO 552

LEAGTH: 939

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.0%; Score 16.8; DB 19; Best Local Similarity 90.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_22019C.1
US-10-437-963-16253
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LOCATION: 419..438
OTHER INFORMATION: 12-65-98.mis1, potential
FEATURE:
Sequence 16253, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 GGACGGTGGAGTCAAGGATT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGAAGGTTGAGTCAAGGATT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: allele
LOCATION: 439
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US-10-741-601-13271/c

US-10-741-601-13271/c

Sequence 13271, Application US/10741601

Publication No. US2004016651941

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: US/10/741,601

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NOWBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

LENOTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9597, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOLSOO
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9597
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                    FEATURE:
NAME/KEY: primer bind
LOCATION: 777..797
OTHER INPORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                               Query Match 82.0%; Score 16.4; DB 21; Length 939; Best Local Similarity 94.4%; Pred. No. 2.7e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.0%; Score 15.8; DB 19; Best Local Similarity 89.5%; Pred. No. 4.7e+02; Matches 17; Conservative 0; Mismatches 2;
LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
                                                                                                                                            ) NAME/KEY: misc_binding

) LOCATION: 427..451

) OTHER INFORMATION: 12-65-98 potential probe

US-10-926-684-552
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; ORGANISM: Homo sapiens
US-10-741-601-13271
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CORGANISM: Homo sapiens
US-10-741-601-9597
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US-10-741-601-9597
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2 GAAGGTTGAGTCAAGGATT 20

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Sequence 130815, Application US/10424599

Sequence 130815, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                            Sequence 23956, Application US/10741600
; Sequence 23956, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
    APPLICANT: CARGILL, Michele et al.
    TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
    TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
    CURRENT APPLICATION NUMBER: US/10/741,600
    CURRENT PILING DATE: 2003-12-22
    CURRENT PILING DATE: 2003-12-22
    NUMBER OF SEQ ID NOS: 73997
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 23956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31551, Application US/10741600
Sequence 31551, Application US/20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILIS REFRENCE: CL001499
FILIS REPRENENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31551
LENGTH: 201
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89.5%; Pred. No. 4.7e+02;
tive 0; Mismatches 2; Indels 0;
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Pred. No. 4.7e+02;
0; Mismatches 2;
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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US-10-741-600-23956
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Best Local Similarity
Matches 17; Conserv
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US-10-741-600-31551/c
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Sequence 23154, Application US/10425115
Sequence 23154, Application US/20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cabou, Youla
APPLICANT: Cabou, Youla
APPLICANT: Cabou, Youla
APPLICANT: Cabou, Youla
APPLICANT: Cabou, Youla
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APPLICANT: Cabou, Youla
APPLICANT: Sabou, Youla
APPLICANT: Sabou, Youla
APPLICANT: 38-315325
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 23154
LENGTH: 367
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Publication No. US20040214272A1

Fublication No. US20040214272A1

Fublication No. US20040214272A1

FUBLICANT: LA FORMATION:

APPLICANT: La Coo, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222) B

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 84482

LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%; Score 15.8; DB 20;
89.5%; Pred. No. 5e+02;
tive 0; Mismatches 2;
                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_89133C.1
US-10-424-599-130815
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US-10-425-115-84482
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130815
LENGTH: 366
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Matches 17; Conservative
                                                                                                                        ORGANISM: Glycine max FEATURE:
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-84482/c
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US-10-425-115-23154/c
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AX774742 Sequence X14768 H. sapiens m

CQ724136 Sequence
AX577974 Sequence
AX577974 Sequence
S1513 monocyte ch
A17786 MCP-1 mRNA.
AR094465 Sequence
E05611 CDNA encodi
AR380620 Sequence
M24545 Human monoc
BC009716 Homo sapi
CQ775689 Sequence
BD195644 70 human
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AR352699 Sequence

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BV166059 CCL2\_498

AC005549 Homo sapi E05599 cDNA encodi

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/note="MAP TO AC005549.1~EXPRESSED IN HELA, SIGNAL = 2.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells
Patent: WO 0157278-A 5501 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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68.2%; Pred. No. 1.7e-24;
ive 50; Mismatches 0; Indels
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Location/Qualifiers
1. 360
/organism="Homo sapiens"
                                                                                                                                                                                                         CQ775688
AR352698
HSJEPR
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Matches 107; Conservative
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CQ069701/c
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TITLE
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CQ2311440 Sequence
AX663646 Sequence
AX663646 Sequence
AX7747 Sequence
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AX69741 Sequence
AX657337 Sequence
AX657317 Sequence
AX657317 Sequence
AX657317 Sequence
                                                                            August 4, 2005, 16:14:42; Search time 996 Seconds (without alignments) 7881.270 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                    4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                SEQ13-8698-9073-50N-TGATCA
162
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CQ218977
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Post-processing:

Database :

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ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT

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S69738 MCP-1=monoc M28226 Human JE ge AR337874 Sequence

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AUTHORS
TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                               /mol_type="unassigned DNA"

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/mole="map TO AC005549.1-EXPRESSED IN PLACENTA, SIGNAL 2.9"
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                                                                                                                                                                                                                                                                                                                                                                                   CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTTCAAGAA
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157216-A 5703 09-AUG-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="MAP TO AC005549.1~EXPRESSED IN BONE MARROW,
                                                                                                                                                Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157272-A 5739 09-AUG-2001;
Acomica, Inc. (US)
Location/Qualifiers
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68.2%; Pred. No. 1.7e-24;
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Sequence 5703 from Patent WO0157276.
CQ135681
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5739 from Patent WO0157272.
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/organism="Homo sapiens"
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Location/Qualifiers
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CQ096880.1 GI:41065906
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Matches 107; Conservative
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RESULT 2
CQ096880/c
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/organism="Homo saplens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/noTe="MAP TO AC005549.1-BXPRESSED IN HEART, SIGNAL = 2.6"
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180, 312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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68.2%; Pred. No. 1.7e-24;
iive 50; Mismatches 0; Indels
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CQ174058
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Location/Qualifiers
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Matches 107; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                             Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human lung
Patent: WO 0186003-A 5889 15-NOV-2001;
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human brain
Patent: WO 0157275-A 5534 09-AUG-2001;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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68.2%; Pred. No. 1.7e-24;
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68.2%; Pred. No. 1.7e-24;
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Sequence 5889 from Patent WO0186003.
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Sequence 5534 from Patent WO0157275.
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/organism="Homo sapiens"
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/organism≃"Homo sapiens"
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CQ294784.1 GI:41255361
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Matches 107; Conservative
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Matches 107; Conservative
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CQ331440/c
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/mol_type="unassigned DNA"
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/note="MAP TO AC005549.1~EXPRESSED IN ADULT LIVER, SIGNAL
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005549:1~EXPRESSED IN FETAL LIVER, SIGNAL
= 3.7"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
August 2000 (03.08.00)<150. GB 24263.6<151. 03 October 2000 (03.10.00.4150. US 60/236,3596151. 27 September 2000 (27.09.00)<150. US 60/236,3596151. 27 September 2000 (27.09.00)<150. US 60/234,6874151. 21 September 2000 (21.09.00)<150. US 09/608,4084151. 30 June 2000 (30.06.00)<170. Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 5816 09-AUG-2001; Acomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
Patent: WO 015/2277-A 5805 09-AUG-2001;
Aeomica, Inc. (US)
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Sequence 5805 from Patent WO0157277.
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Best Local Similarity 68.2<sup>3</sup>
Matches 107; Conservative
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Human JE gene encoding a monocyte secretory protein, exon 3.
M28225 M26035
M28225.1 GI:339005
                                                                                                                                                                                                                                                                                                                                               Genes and proteins for prevention, prediction, diagnosis, prognosis and treatment of chronic lung disease Patent: WO 02097127-A 21 05-DEC-2002; Bayer Aktiangesellschaft (DE)
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Rollins; B.J., Stier,P., Ernst,T. and Wong,G.G. The human homolog of the JE gene encodes a monocyte secretory
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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               CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGCTTCAGGA
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                                                                                                                                                                                                     linear
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                                                                                                                 protein
Mol. Cell. Biol. 9 (11), 4687-4695 (1989)
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                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 21 from Patent WO02097127.
AX663646
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Matches 107; Conservative
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HUMSECP3
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/product="monocyte secretory protein"
/product="monocyte secretory protein"
/protein_id="AaA60308.1"
/db_xref="ed1:338007"
/db_xref="ed1:338007"
/translation="wkycspalicitlinampripoglaoppainapyrccynFTNRKIS
vorlaAsyrrisskcpkeaviFkTIVakEICadpkQkwvQDSmDHLDKQTQTPKT"
join(M28223.1:669. .675,M28224.1:1. .118,1. .103)
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To (bases 1 to 478)
Rollins, B.J., Stier, P., Ernst, T. and Wong, G.G.
Unpublished (1989)
Original source text: Human lung fibroblast W138 cell line, DNA,
clones hJE-34 and lambda-hJE-7.
[2] sites for [1].
Draft entry and computer readable sequence for [1] kindly provided
by B.J.Rollins 17-JUL-1989.
Location/Qualifiers
1. 478
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                     /organism="Homo mapiens"
/organism="Homo mapiens"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db for 1 line="W138"
/cell line="W138"
/cell type="fibroblast"
/tissue type="lung"
join (W28223.1:532. .675,M28224.1:1. .118,1. .478)
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|oin(M28223.1:600. .675,M28224.1:1. .118,1.
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Methods for assessing and treating leukemia
Patent: WO 03038129-A 97 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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Sequence 97 from Patent WO03038129.
AX774781
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/mol_type="unassigned DNA"
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ilarity 68.2%;
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/gene="JE"
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Matches 107;
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PAT 08-OCT-2004
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Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
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Charge tags and separation of nucleic acid molecules
Patent: WO 02063030-A 72 15-AUG-2002;
THIRD WAYE TECHNOLOGIES, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 254
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Best Local Similarity 68.2%; Pred. No. 1.9e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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                       ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
                                          126 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT
                                                                                                                                           RNA
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                                                                                                                                       AR567996 647 bp 18
Sequence 72 from patent US 6780982.
AR567996
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/wol_type="unassigned RNA"
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Best Local Similarity 68.2%
Matches 107; Conservative
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synthetic construct
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VQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQTQTPKT"
                                                                                                                                                                                                                                                                                                                                                                                   PRI 23-MAY-1994
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1 (bases 1 to 48: Primates; Catarrhini; Hominidae; Homo.
Rollins, B.J.; Stier, P., Ernst, T. and Wong, G.G.
The human homolog of the JB gene encodes a monocyte secretory
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                                                                                                                                       1 CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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join[M30816.1:600. .675, M31625.1:6. .123,6. .111)
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                                                 Length 482;
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Human monocyte secretory protein (JE) gene, exon 3.
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Best Local Similarity 68.2%; Pred. No. 1.8e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
                                                                                   Indels
                                                                                                                                                                                                                                                                             126 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 162
                                                                                                                                                                                                                                                         'note="monocyte secretory protein"
                                                 ; Score 157; DB 6; L; Pred. No. 1.8e-24; 50; Mismatches 0;
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Unknown number of bp after segment 2.
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/note="MSP, intron B"
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Location/Qualifiers
1. 482
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                                                 Query Match
Best Local Similarity 68.2%;
Matches 107; Conservative 5
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Homo sapiens
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1 (bases 1 to 661)
Horwitz,K.B. and Richer,J.
Progesterone receptor-regulated gene expression and methods related thereto
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                                                                                                                                                                                             linear PAT 08-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 CTTCAAGACCATTGTGGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGAGGGTTCAGGA 285
                            61 TICCAIGGACCACCIGGACAAGCAAACCCCAAACTICGAAGACTIGANNNNNNNNNNNNNN 120
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195 CITCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 254
                                               255 TTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACTTGAACACTCCACA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Location/Qualifiers
1. .61
/organism="unknown"
/mol_type="genomic DNA"
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Sequence 104 from patent US 6750015.
AR59337 GI:53968753
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AAI15568 standard; DNA; 360 BP.
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1 cttcaagaccattgtggcca.....nnnnnnnnnnnnntgatca 162
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aai15568 Probe #55	Aba57500 Human foe	Aai37053 Probe #57	Aba26988 Probe #54		Aak05543 Human bra	Abs30826 Human liv	Abs05898 Human gen	Abv96715 Human pan	Abv97697 Human pan	Acc46770 Human COP	Adn95619 Human BEC	Adpl3526 Renal cel	Ade84878 Farnesyl	Abs68800 Human mon	Aaa74882 Human che	Aag85370 Chemoattr	Aax80631 Monocyte	Aad58817 Human mon	Add18494 Human pro
SUMMARIES	ΩI	AA115568	ABA57500	AA137053	ABA26988	AAK31146	AAK05543	ABS30826	ABS05898	ABV96715	ABV97697	ACC46770.	ADN95619	ADP13526	ADE84878	ABS68800	AAA74882	AAQ85370	AAX80631	AAD58817	ADD18494
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells. Probe #5501 for gene expression analysis in human cervical cell sample. Probe; human; microarray; gene expression; cervical epithelial cell; Rank DR; 04-FEB-2000; 2000US-0180312P. 26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-0608408. 03-AUG-2000; 2000US-00533366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0234359P. 04-OCT-2000; 2000GB-00024263. (MOLE-) MOLECULAR DYNAMICS INC. Chen W, 30-JAN-2001; 2001WO-US000670. Hanzel DK, cervical cancer; ss. WPI; 2001-488901/53. WO200157278-A2. Homo sapiens. 09-AUG-2001. Penn SG, RESULT 1
AAI15568/C
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AC AAI155
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(first entry)

The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon

Claim 25; SEQ ID NO 5501; 487pp; English.

at ftp.wipo.int/pub/published\_pct\_sequences

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n genome-derived single exon nucleic acid probes useful for analyzing expression in human fetal liver.
                                                                                                                                                                                                                                                                             foetal liver; gene expression; single exon nucleic acid probe; ss.
microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                 1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human foetal liver single exon nucleic acid probe #5805.
                                                                                                                        Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
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                                                                                                                     299
                                                                                                                                             298 TICCAIGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCCACA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                              1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                    Probe #5739 used to measure gene expression in human placenta sample.
                                                                     Gaps
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llarity 68.2%; Pred. No. 0.73;
Conservative 50; Mismatches 0; Indels
                                            Length 360;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                           Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                 Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
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                                          96.9%; Score 157; DB 4;
68.2%; Pred. No. 0.73;
iive 50; Mismatches 0.
                                                                                                                                                                                                                   ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 5739; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human placenta.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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ID AAI37053 standard; DNA; 360
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                                                                         Conservative
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Matches 107; Conserv
                                               Query Match
Best Local Similarity
Matches 107; Conserv
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358 CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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21-SEP-2000;
27-SEP-2000;
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AAK31146/
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                                  299
                                                                                    TTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCACACA 239
                                                               Single exon nucleic acid probes for analyzing gene expression in human
                    CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                              Probe #5454 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                             ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 5454; 530pp; English.
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30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease; ss
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1 CITCAAGACCAITGIGGCCAAGGAGAICIGIGCTGACCCCAAGCAGAAGTGGGITCAGGA 60

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
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cricaagaccarrereccaaggagarcrerecreaccccaagcagaagregerreagga
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microarray; cancer; leukaemia; lymphoma; myeloma; 88.
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                                                                                                                                                   202
                                                                                              238 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression in human bone marrow.
                                                                                                                                                                                                                                                                            AAK31146 standard; DNA; 360 BP
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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Pred. No. 0.73;
0; Mismatches 0; Indels
                                                                                                                                                         Human brain expressed single exon probe SEQ ID NO: 5534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                     BP.
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2000US-00608408.

2000US-00632366.

2000US-0234687P.

2000US-0236359P.
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                                                                                     AAK05543 standard; DNA; 360
                                                                                                                                      (first entry)
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Best Local Similarity
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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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                                                                                                             AAK05543;
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nuclectide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be in samples derived from human adult liver. The genes identified may be in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, byperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS5105 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at Epp. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                            Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
                                                                                                                                                                            Human liver single exon probe, SEQ ID No 5816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.2%; Pred. My.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 5816; 658pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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ABS30826/c
ID ABS30826 standard; DNA; 360
                                                                                                                                 (first entry)
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les 107; Conservative
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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03-AUG-2000;
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                                                                                                                                 25-FEB-2003
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                                                                          ABS30826;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements or the 12887 open reading frames derived from the 12614 complements or the 12887 open reading frames derived from the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the 12614 complements or the numan lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the algorithmically predicting at least one exon from genomic sequences of the eukaryotte; and (b) detecting specific hybridisation of detectably comprising (a) included microarray, assigning exons to a single exon probe, having a fragment identical to the predicted exon, the probe is included to the above and (b) measuring the expression of each of the exons in several comprising (b) measuring the expression of each of the exons in several comprising on the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising on the exons should be assigned to a single gene, a peptide comprising on the exons should be assigned to a single gene, a peptide comprising on the exons should be assigned to a single gene, a peptide comprising on the exons should be assigned to a single specification, or encoded by the
                                                                                                                                                                                                                    Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                          Human genome-derived single exon probe from lung SEQ ID No 5889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measure gene expression in human lung samples.
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                            ABS05898 standard; DNA; 360 BP.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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                                                                                                                         (first entry)
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                                                                                                                         19-AUG-2002
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                                                                        ABS05898;
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ABS05898/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The probes are used for gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                 Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cricaagaccarreresccaaggagarcrerecteaccccaagcagaagregerreaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 157; DB 6
Fred. No. 0.73;
50; Mismatches
probes/open reading frames (ORF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV96715 standard; cDNA; 473 BP
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; 2001US-0305484P.;
; 2001US-0313999P.;
; 2001US-0333626P.
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68.2%;
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2001US-0278651P.
2001US-0287112P.
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2001US-0265682P.
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Best Local Similarity
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27-NOV-2001;
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21-MAR-2001;
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                                         The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately cresidues of (a); (d) sequences having at least 75 or 90% identity of tringent conditions; (e) sequences having at least 75 or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-C) abre6837) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour CC polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the primed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                               CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 60
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pancreas; cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss.
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                                                                                                                                                                                                                                                                                    96.9%; Score 157; DB 6; Length 473; 68.2%; Pred. No. 0.8;
                         Claim 1; SEQ ID NO 2123; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                             Sequence 473 BP; 129 A; 121 C; 89 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic cancer expressed cDNA SEQ ID NO 3105.
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
                                                                                                                                                                                                                                                                                                              50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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20010S-0267568P.
20010S-0278651P.
20010S-029112P.
2001US-031648P.
2001US-0313999P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV97697 standard; cDNA; 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                  Best Local Similarity 68.23
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200260317-A2.
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09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV97697;
                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                         Query Match
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ABV97697/c
     cancer
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences that hybridize to (a), under moderately cresidues of (a); (d) sequences that hybridize to (a), under moderately creditions: (e) sequences having at least 75 or 90% identity citingent conditions: (e) sequences having at least 75 or 90% identity citingent conditions: (e) leadents of (a). Polypeptides (ABP68596-C) an a patient and compositions complising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and composition of ribozyme molecules for inhibiting expression of the tumour CC proparation of ribozyme molecules for inhibiting expression of the tumour cc propagation of ribozyme molecules for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chronic obstructive pulmonary disease; COPD; chronic lung disease;
                                                                      New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3105; 300pp + Sequence Listing; English.
Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 475 BP; 134 A; 90 C; 122 G; 129 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 123
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC46770 standard; cDNA; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity 68.2
Matches 107; Conservative
   Kalos MD,
                                                          WPI; 2002-627435/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200297127-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2003
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      Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC46770;
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Example 1; SEQ ID NO 542; 176pp; English.
              WPI; 2003-876899/81.
                           P-PSDB; ADN95618
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                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCATGGACCACCTGGACAAACCCAAACTCCGAAGATTGAACACCCACTCCACA 120
                                                                                                                     The present invention describes a method for predicting, diagnosing or prognosing chronic lung disease by detecting a chronic obstructive pulmonary disease (COPD) gene related polymucleotide (see ACC46750 to ACC46777, which encode the COPD related porterins in ABP96779 to ABP96806). The method is useful for predicting, diagnosing or prognosing chronic lung disease in a biological sample. The COPD genes and proteins encoded by them from the present invention (I) can be used for treating or preventing chronic lung disease in a mammal. (I) can be used in an animal model for determining the efficacy, toxicity, or side effects of treatment with (I), and determining the mechanism of action of (I). ACC46778 to ACC46903 represent COPD related PCR primers and probes used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting, diagnosing or prognosing chronic lung disease, by detecting a chronic obstructive pulmonary disease (COPD) gene in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth, differentiation, blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGFC; VEGF-D; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
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                                                                                                                                                                                                                                                                                                                                                                1 CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                          1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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Hall R, Schulze T, Kroegel
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                                                                                                                                                                                                                                                                                                              96.9%; Score 157; DB 10; Length 478; 68.2%; Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                       Sequence 478 BP; 142 A; 91 C; 78 G; 167 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BEC/LEC-related gene sequence SeqID542.
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 68.2%; Pred. No. 0.81
Matches 107; Conservative 50; Mismatches
Kallabis H,
                                                                                                Claim 8; Page 110; 214pp; English.
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Gehrmann M,
                       WPI; 2003-140492/13.
P-PSDB; ABP96799.
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Oellers N,
                                                                                                                                                                                                                                                                                                                 Query Match
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic conductial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or composition comprising an agent that differentially modulates blood or composition comprising a LEC protein, where the mutation in at least one allele of a gene encoding a LEC protein, where the mutation in at cleat one allele of a gene encoding a LEC protein, where the mutation in at composition comprising a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 478 BP; 142 A; 91 C; 78 G; 167 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Twine NC, Sloni DK;

Sloni

(DORN/) I (STOV/) S (SLON/) S

(AMHP) (BURC/) (TREP/)

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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(IB)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TICCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCCACA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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farnesyl transferase inhibitor; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.9%; Score 157; DB 10; Length 482; 68.2%; Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human monocyte chemoattractant protein-1 (hMCP-1) RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 97; 346pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
          ss; cytostatic; farnesyl trans
quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                             30-OCT-2002; 2002WO-US034784.
                                                                                                                                                                                                                                                                                                                                                          30-OCT-2001; 2001US-0338997P.
30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
30-OCT-2001; 2001US-0341012P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS68800 standard; RNA; 647
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Matches 107; Conservative
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                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raponi M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relate to a method of diagnosing (MI) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the cannot be compared to the genes is differentially expressed in peripheral compared to PBMCs of normal humans. The method is useful for diagnosing compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from non-blood disease such as solid tumor. The solid tumor is chosen from non-blood disease such as solid tumor. The solid tumor is chosen from sample is a whole blood sample (claimed). (MI) is useful for identifying genes that are differentially expressed in peripheral blood sample is solated at differentially expressed in peripheral blood sample is solated at differentially expressed in peripheral blood sample is solated at differentially expressed in peripheral blood sample is solated at differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification but was obtained from WIPO in electronic format at the wipo./pub/published_pot_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTTCAAGACCATTGTGGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dorner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 157
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50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trepicchio WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 262; 350pp; English.
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                                                            21-NOV-2003; 2003WO-US037481.
                                                                                                                        21-NOV-2002; 2002US-0427982P.
03-APR-2003; 2003US-0459782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.2<sup>3</sup>
Matches 107; Conservative
                                                                                                                                                                                                                                                 TWINE N C.
BURCZYNSKI M E.
TREPICCHIO W L.
DORNER A.
STOVER J A.
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RESULT 14 ADE84878

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The invention relates to a composition comprising a positively or neutrally charged phosphoramidite. The composition is useful for neutrally charged phosphoramidite. The composition is further useful for for fraction at nucleic acid molecules. The composition is further useful constraint of incleic acid molecules. The specific nucleic acids by selective charge reversal useful in e.g. INVADER assay cleavage reactions; and in the synthesis of charge-balanced molecules in the fractionation of nucleic acid constructes, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the cuse of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate. ABS68740.
                                                                                                                                                                                                                                                                                                                                           Composition useful for e.g. separation of nucleic acids comprises a positively or neutrally charged phosphoramidite.
                                                                                                                                                                                                                                           Wayland SR, Takova T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 647 BP; 180 A; 146 C; 121 G; 0 T; 200 U; 0 Other;
                                                                                                                                                                                                                                      Lyamichev V, Skrzpczynski Z, Allawi HT,
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 14; Page 194; 197pp; English
                                                                                                                                                                                            (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                         06-FEB-2002; 2002WO-US003423.
                                                                                                                                                 06-FEB-2001; 2001US-00777430.
                                                                                                                                                                                                                                                                                                        WPI; 2002-674850/72.
                      WO200263030-A2.
                                                                 15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                               Neri BP;
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315 ACCCAAGAAUCUGCAGCUAACUUAUUUUCCCCUAGCU 351 g ð

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1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 60

Query Match 96.9%; Score 157; DB 6; Length 647; Best Local Similarity 55.4%; Pred. No. 0.89; Matches 87; Conservative 70; Mismatches 0; Indels

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	AV661469 AV661469	N28510	A1478647 tm54f08.	CD673147	AV71455	BG236324	BF11513	CK90213	BF59062	AW96701	BX490080	BM70491	AA61452	BF08163	AI692798	AV735130	BP19703	AA877558	BE326715	BM997526	BM70861	AW59411	BM88825	BQ63144
SUMMARIES	а	AV661469	N28510	A1478647	CD673147	AV714555	BG236324	BF115131	CK902135	BF590622	AW967017	BX490080	BM704915	AA614521	BF081639	A1692798	AV735130	BP197032	AA877558	BE326715	BM997526	BM708613	AW594110	BM888255	BQ631442
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	& Query Match	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9	96.9
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Query Match 96.9%; Score 157; DB 1; Length 432; Best Local Similarity 68.2%; Pred. No. 1.1e-21; Matches 107; Conservative 50; Mismatches 0; Indels

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BU069097 im57d11.x CT370829 TGBSTZxyj5 CK902136 i117e04.y BUS80378 in333b12.x BUS80675 in36903.x AL697816 DKFZD686E AV716988 AV716988 AW773803 xx24b04.x AW772091 hn67c08.x BU730951 UI-E-CII- AV713706 AV713706 BQ631169 i117e04.x AV717017 AV717339 BM85551 UI-E-CII- BM873445 UI-CF-ECI BU688561 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI BU688564 UI-CF-ECI	SNTS	AV661469  AV6614	
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                                                          241 CTTCAAGACCATTGTGGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 300
                                            Email: est@watson.wustl.edu
High quality sequence stops: 305
Source: IMAGE Consortium, LINL.
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                           361 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 397
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96.9%; Score 157; DB 7; Length 446; 68.2%; Pred. No. 1.1e-21; ive 50; Mismatches 0; Indels

Query Match Best Local Similarity 68.2 Matches 107; Conservative

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/clone llb="NCIC GAP Kidl1"
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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: Kidney; Vector: pT81; Site 2: BCO RI;
a modified polylinker; Site 1: Not I; Site 2: BCO RI;
plasmid DNA from the normalized library NCI CAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132276-1323911, 1456007-1456775, and
150052-150255). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Procurement: Christopher Moskaluk, M.D., Ph.D., Contact Library Preparation: M. Bento Soares, Ph.D.
Contact Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NOT-CGAP clone distribution information can be found through the 1.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/laage/hmage.html
Insert Length, M.D. Std Error: 0.00
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tm54F08.x1 NCI CGAP Kidl1 Homo sapiens cDNA clone IMAGE:2161959 3'
similar to gb:W24545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -400P from Gibco
High quality sequence stop: 444.
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AV714555 DCB Homo sapiens cDNA clone DCBADG05 5', mRNA sequence.
AV714555 LG GI:10796072
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                                      259 crrchagaccarreredeccaagaagarcrerecreaccecaagcagaagreega 318
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(bases I to 513)

Xu,X., Gu,J., Liu,F., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Homo sapiens CDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801319(ex.45)
Fax: 86-21-50801922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                 250 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 286
                                                                                                                          ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 415
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/mol type="mRNA"
/do xefe="exaon:9606"
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/tissue_type="Iris"
/dev stage="Addlt"
/dev stage="Addlt"
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/clone_lib="Human Iris cDNA (Normalized): fg"
/clone_lib="Human Iris cDNA (Normalized): fg"
/clone_lib="Human Iris cDNA (Normalized): fg"
/clone_lib="Human Iris cDNA (Normalized): fg"
/clone_lib="Human Iris cDNA (Normalized): fg"
/clone_lib="man iris convalidated by as liberary (bx) was normalized by self-subtraction. One portion of double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonucleases III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (COt 500) with 41 mg of Blo-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/8s-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural
                                                                                                                                                                                                                                                                                                               Los/1147 Ser 24-JUN-2003 FRNA linear EST 24-JUN-2003 [421d04.yl Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapiens cDNA clone sapien
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llarity 68.2%; Pred. No. 1.2e-21;
Conservative 50; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                           362 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 326
                                                                                                                       Email: graeme@helix.nih.gov
Plate: 21 row: d column: 04
Seq primer: M13Rb1 reverse primer (ABI).
Location/Qualifiers
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Mol. Vis. 8 (4), 185-195 (2002)
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Homo sapiens
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Mammalia; Eutheria;
1 (bases 1 to 506)
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Fax: 301 496 0078
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                                                                                                                                 Tumor Gene Index
I Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D. and M.Fatima
CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.lln! gov
Seq primer: -40UP from Gibco
High quality sequence stop: 425.
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1 (bases 1 to 541)
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. thases 1 to 520. NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="lymphocyte"
/lab_host="DM10B (phage-resistant)"
/clone_lib="Sacres NPBM"
/note="Organ: blood; Vector: pT7T3D-Pac; Site_1: Not1;
Site_2: EcoRI; 1st strand cDNA was primed with a Not I
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/mol type="mRNA"
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BF115131.1 GI:10984607
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                    Homo sapiens (human)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoamage.llh.gov
Seq primer: -400P from Gibco
High quality sequence stop: 471.
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/clone_lib="NCI CGAP_Kidl1"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site=1: Not 1; Site=2: ECO RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hypridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5.000 clones made from the same library
(cloneIDs 13223/6-1323911, 1456007-1456775, and
Fatima Bonaldo. "Subtraction by Bento Soares and M.
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1 (bases 1 to 542)

Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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68.2%; Pred. No. 1.3e-21;
Live 50; Mismatches 0;
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:3134266"
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                                                                            Tumor Gene Index
Unpublished (1997)
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AW967017.1 GI:8156853
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AW967017
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                                                                                                                                                                                                                                   Good hit to opposite strand read. ..wrong orientation BUT PASSED FOR MOUSE-PANCHEAS VERIFICATION
POSSIble reversed clone: smilarity on wrong strand
Seq primer: -40RP from Glood
High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7440h06.x1 NCI CGAP CO16 Homo sapiens cDNA clone IMAGE:3318491 3' similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 BFS90622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site_1: Not1; Site_2: XhoI; CNNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoueeàmgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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                  Other ESTS: ill7e04.yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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                                                                                                                                  Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
This read is a 3' RESEQUENCE of a previously sequenced pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:6030414"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
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                                                                                                                                                                                                                                                                                                                                                          1. .542
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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  Unpublished (2000)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDN Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Linu, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="NCI CGAP_COL6"
/clone lib="NCI CGAP_COL6"
/note="Organ: Colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Bco RI, Plasmid DNA from the normalized library NCI CGAP COl0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351)
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EST379091 MAGE reseguences, MAGJ Homo sapiens CDNA, mRNA seguence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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Uppublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: Johng@tigr.org
Plate: 235
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metastasis using a 19,200 element cDNA microarray
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/mol_xref="taxon:9606"
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DKFZp686B1371_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone
DKFZp686B1371_r', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Gerome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGeromix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
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                                                                                                                                                                                                                                                                                                                               298 TICCAIGGACCACCTGGACAAGCAAACCCGAAGACTTGAAGACTTGAAGACTCCACA 357
                                                                                                                                                                                                                                                                                             238 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 297
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Cytenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Site_1: SfiIA, Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp686B1371) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
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/noce="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                                                           358 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 394
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/lab_host="DH10B"
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       Location/Qualifiers
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Homo sapiens
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Best Local Similarity 68.2%
Matches 107; Conservative
Seg primer: Reverse
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Unpublished (2003)
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Gaps

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/mol type="mRNA"
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// db xref="taxon:966"
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 9565
Email: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seg primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM704915
UI-E-CII-agf-h-04-0-UI.rl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CII-agf-h-04-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 563)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
     9
CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                   383 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 419
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1 (bases 1 to 565)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asingeon@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR0-AN0084-190 900-0002-f07kf3=2000-00-19&t4=1)
Seq primer: puc 18 forward Seq primer: puc 18 forward High quality sequence stop: 374.
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MRO-AN0084-190900-002-£07 AN0084 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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      0; Indels
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      Mismatches
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BF081639.1 GI:10875469
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BF081639
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Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmart-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 811 Std Error: 0.00
Seq prime: -40m13 fwd. ET from Amersham

High quality sequence stop: 10cation/Qualifiers
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/issue type="breast"
/lab.host="bH10B"
/clone lib="NOI CAAP Br1.1"
/clone lib="NOI CAAP Br1.1"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. (The normalized
version of this library is NOI CCAP Br2.) Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                              Length 563;
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Pred. No. 1.3e-21;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1129617"
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AA614521.1 GI:2466717
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time : 1657 secs

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Job
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: capbs-remail.nih.gov
Life Technologies catalog #: 11548-013
Life Technologies catalog #: 11548-013
Location distribution by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 707 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
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                                                   323 TICCATGGACCACCTGGACAAGCAAACCCCAAAGACTTGAACATTCACTCCACA 382
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 569)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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96.9%; Score 157; DB 1; Length 569;
Best Local Similarity 68.2%; Pred. No. 1.3e-21;
Matches 107; Conservative 50; Mismatches 0; Indels
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                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .569
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2325299"
                                                                                                                                                                                                                                                                                                                            AI692798.1 GI:4970138
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                            RESULT 15
AI692798/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
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COMMENT
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Search completed: August 4, 2005, 17:38:36

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Sequence 104, App
Sequence 3, Appli
Sequence 1344, Ap
Sequence 25, Appl
Sequence 1165, Ap
Sequence 106, App
Sequence 106, App
Sequence 106, App
Sequence 106, App
Sequence 105, App
Sequence 106, App
Sequence 105, App
Patent No. 5212073
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                                                                                                                                August 4, 2005, 16:44:28; Search time 83 Seconds (without alignments) 3193.697 Million cell updates/sec
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                                                                                                                                                                                                                                                                           cttcaagaccattgtggcca.....nnnnnnnnnnnntgatca
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-3840
US-07-927-391-15
US-09-949-016-15582
US-09-36-887A-21
US-09-577-204-21
US-09-516-887A-26
US-09-366-887A-26
US-09-366-887A-26
US-09-03-65-978
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US-09-814-915A-104
US-09-591-992-3
US-09-023-655-1344
US-07-927-391-25
US-08-437-306-1
US-08-437-306-1
US-09-148-545-106
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-09-016-434-687
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                                                                                                                                                                                                                                                                                                                                                                                             1202784 segs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                     SEQ13-8698-9073-50N-TGATCA
162
1 cttcaaqaccattotograa
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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994
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Perfect score:
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US-09-545-894-1 US-09-016-434-1033

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RESULT 2
US-09-814-915A-104

Sequence 104, Application US/09814915A

Pacent No. 6750015

GENERAL INFORMATION:

APPLICANT: Horwitz, Kathryn

APPLICANT: Richer, Jennifer

TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Related
                                                                                                                                                                                          Appli
                                                                                                                                                                                                                                                                                                                                                                                            CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                      Sequence 38,
Sequence 44,
Sequence 2,
                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NWINNWINNWINNWINNWINNWINNWINNWINNWIN 157
US-09-545-894-3

US-08-744-419-1

US-09-366-814-15

US-09-463-451-29

US-09-463-451-29

US-09-463-451-29

US-09-646-028-37

US-09-646-028-37

US-09-646-028-38

US-09-646-028-45

US-09-646-028-45

US-09-646-028-45

US-09-646-028-41

US-08-250-958-3

US-08-250-958-3

US-08-250-958-3

US-08-250-958-1

US-08-1568-1

US-08-1568-1

US-09-044-8568-1
                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic US-09-777-430C-72
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.4*
Matches 87; Conservative
 514
818
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360
         RESULT 1
US-09-777-430C-72
 112.8
112.8
109.2
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109
100
107.4
1005.6
1005.4
101.8
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990.4
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JS-09-023-655-1344
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APPLICANT: Devico, Anthony L.
APPLICANT: Garzino, Alfedo
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE REPERENCE: 4115-109 CIP
CURRENT APPLICATION NUMBER: US/09/591,992
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: PCT/US98/26291
PRIOR APPLICATION NUMBER: US 60/186,416
PRIOR PLING DATE: 1998-12-11
PRIOR PELING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/069,281
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 725
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                                                                                                                                                                                                                                                96.9%; Score 157; DB 4; Length 661; 68.2%; Pred. No. 0.014; ive 50; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRICR APPLICATION NUMBER: 60/214,870
PRICR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 104
LENGTH: 661
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US-09-591-992-3
; Sequence 3, Application US/09591992
; Patent No. 6569418
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Best Local Similarity 68.2*
Matches 107; Conservative
Thereto
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APPLICANT: Gallo, Robert C.
                                                                                                                                                                                                                                                                       Best Local Similarity 68.2
Matches 107; Conservative
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                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
TITLE OF INVENTION:
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                                                                                                                              FOR THE DETECTION OF BLOOD CELL GENE
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                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSERFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETH
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESSS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
; Sequence 1344, Application US/09023655; Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/07927391; Patent No. 600169 GENERAL INFORMATION: APPLICANT: CAPUT, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELBETAK: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 725 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                   CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LIBRARY: GENB<sup>1</sup>; CLONE: 934513
US-09-023-655-1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                     94304
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US-07-927-391-25
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264 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTTCAGGA 323
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68.2%; Pred. No. 0.015;
.ive 50; Mismatches 0; Indele
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Patent No. 6787645

GENERAL INFORMATION:

APPLICANT: Stiles, Charles D.

APPLICANT: Wong, Gordon G.

ITLE OF INVENTION: No. 6787645el Human Cytokine

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: HERENITH (125,055)
FILING DATE: HERENITH (125,055)
FILING DATE: APPLICATION:
FILING DATE: CLASSIFICATION WIMBER:
FILING DATE: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0001 US
REFERENCE/DOCKET NUMBER: PA-0001 US
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 68.2*
Matches 107; Conservative
      CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: GENBANK
; CLONE: 9187434
US-09-023-655-1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: lin
                                           USA
                                                                  94304
                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-08-437-306-1
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                                                     APPLICANT: VITA, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                     ADDRESSEE: FULE & LARGUNEK
STREET: King Street Station, Suite 500,1800 Diagonal
GITY: ALEXANDRIA
STREET: Road,PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
COMPUTER: LEAP PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MA-DOS
SOFTWARE: 19920929
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: SAKE, BETCHAID
REGISTRATION NUMBER: 28,665
REPERENCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT 420
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: COMPOSITION FOR THE DETRITILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
MILOUX, Brigitte
MINTY, Adrian
VITA, Natalio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.2
Matches 107; Conservative
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
                                                               R APPLICATION NUMBER: 60/040,336
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,163
R FILING DATE: 1997-05-03-07
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
                                                                                                                                                                                                  R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R PELING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-04-11
APPLICATION VUMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-23
APPLICATION VUMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
APPLICATION NUMBER: 60/047,584
APPLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/047,587
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
  FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 423
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

JETLE OF INVENTION: 70 Human Secreted Proteins
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT PILING DATE: 1998-09-04
FEARLIER PILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER PILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
96.9%; Score 157; DB 4;
Best Local Similarity 68.2%; Pred. No. 0.015;
Matches 107; Conservative 50; Mismatches
                                   CURRENT APPLICATION DATE:

CURSENT APPLICATION NUMBER:

CLASSTRICATION NUMBER:

CLASSTRICATION 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/228,931

PILING DATE: 13-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/003,136

FILING DATE: 12-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,515

FILING DATE: 12-JAN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,515

FILING DATE: 12-MAY-1991

FILING DATE: 12-MAY-1991

FILING DATE: 12-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: BROOK, David E.

REGISTRACTION VUMBER: 2,592

REFERENCE/DOCKET NUMBER: 2,592

REFERENCE/OCKET NUMBER: 2,592

REFERENCE/OCKET NUMBER: 2,593

REJERPAX: (617) 861-6240

TELECOMONICATION INFORMATION:

TELEPAX: (617) 861-6240

TELEPAX: (617) 861-6240

TELEPAX: (617) 861-6240

TELEPAX: (617) 861-6240

TELEPAX: (617) 861-6240

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TELEPAX: (617) 861-6240
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Patent No. 6590075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
73..369
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, LOCATION:
US-08-437-306-1
       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
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ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/056,886
ER APPLICATION NUMBER: 60/056,886
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,893
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,893
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,878
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R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,864

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

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R APPLICATION NUMBER: 60/056,845

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R APPLICATION NUMBER: 60/056,892

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R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/047,595

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-06-23

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

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RR APPLICATION NUMBER: 60/056,890
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 APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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FILE REFERENCE: P2001P1
CURRENT PILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PC/1/US98/04482
EARLIER FILING DATE: 1998-03-06
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EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
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Patent No. 6590075
GENERAL INFORMATION:
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Best Local Similarity
Matches 107; Conserv
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LENGTH: 1712
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R APPLICATION NUMBER: 60/047,591
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R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
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R FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
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R PILING DATE: 1997-04-11
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R FILING DATE: 1997-04-11
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R PILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
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R FILING DATE: 1997-03-07
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R FILING DATE: 1997-05-23 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
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APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/056,845 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER EARLIER EARLIER EARLIER EARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: DATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACUTICALS, INC.
STREET: 3174 PORTER DRIVE
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5212073-1
; Patent No. 5212073
; Patent No. 5212073
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
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86.4%; Score 140; DB 6; Length 752;
Best Local Similarity 61.5%; Pred. No. 0.32;
Matches 96; Conservative 50; Mismatches 10; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                         387 CTGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGA 422
                                                                                                                                        CTGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGA 422
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FILING DATE:12-MAY-1989
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION:
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STATE: CALIFORNIA
COUNTRY: USA
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CLASSIFICATION:
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Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROLLINS, BARRETT;STILES, CHARLES;WONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 140; DB 6; Length 752; 61.5%; Pred. No. 0.32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Mismatches
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER PILING DATE: 1997-08-22
EARLIER PELLONTON NUMBER: 60/056,908
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER PILING DATE: 1997-09-05
EARLIER PILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
                                                                                  ER APPLICATION UNDER: 60/047,501
ER PILING DATE: 1997-05-23
ER PLING DATE: 1997-05-23
ER PLING DATE: 1997-06-11
ER PLING DATE: 1997-08-22
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,664
ER PILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,816
ER PLING DATE: 1997-08-22
ER PLING DATE: 1997-08-22
ER PLING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
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ER PELING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
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ER PELING DATE: 1997-08-22
                                          APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
60/043,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008
FILING DATE:12-MAY-1989
APPLICATION NUMBER: 60/
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%;
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Best Local Similarity 68.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5212073
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LENGTH: 1822
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385 ACTGAAAACAAGCCATGACTTGAGAAACAAATAATTTG 422
                                                                                                                                                                                                                                                                         APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: MILOUX, Adrian
APPLICANT: MINTY, Adrian
APPLICANT: WITA, Natalio
TITLE OF INVENTION: Protein ha
TITLE OF INVENTION: for its pr
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 814 base pairs
NUCLEIC ACID
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Best Local Similarity 58.2
Matches 92; Conservative
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41..139
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140..367
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LENGTH: 814 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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, LOCATION:
US-07-927-391-15
                                                                                                                                                                 US-07-927-391-15
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| Sequence 3840, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT VENTER. VENTER. VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VENTER VE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.7%; Score 132.4; DB 4;
58.2%; Pred. No. 1.3;
ive 50; Mismatches 16;
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NAWE: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPEREENCE/DOCKET NUMBER: PA-007
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-055
TELEPHONE: (650) 845-055
INFORMATION POR SEQ ID NO: 1273:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
STRANDEDRESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LINEARY: GENBANK
LINEARY: GENBANK
SCHORE: 9288396
US-09-016-434-1273
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Best Local Similarity 58.2'
Matches 92; Conservative
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Best Local Similarity
Matches 92; Conserv
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ORGANISM: Human
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Protein having a cytokin type activity, and recombinant DNA, expression vector and hosts for its preparation.
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                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/927,391

FILING DATE: 1992099

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhart 28,665

REGISTRATION NUMBER: 16781/369

TELERENCE/DOCKET NUMBER: 16781/369

TELERENCE/DOCKET NUMBER: 16781/369

TELERENCE/TONIN NUMBER: 16781/369

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TELERENCE/TONIN NUMBER: 16781/369
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA
COUNTRY: USA
ZIP: 22319-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 15, Application US/07927391; Patent No. 6001649; GENERAL INFORMATION:
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Sequence 15582, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TATLE OF INVENTION: OCIMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
FRICK APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR FLING DATE: 2000-10-3
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15582
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81.7%; Score 132.4; DB 4; Length 6022;
Best Local Similarity 58.2%; Pred. No. 4.6;
Matches 92; Conservative 50; Mismatches 16; Indels 0;
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                                                              385 ACTAAAAACAAGCCATGACTTGAGAAACAAATAATTTG 422
Search completed: August 4, 2005, 17:40:05 Job time: 84 secs
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; ORGANISM: Human
US-09-949-016-15582
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US-09-949-016-15582
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August 4, 2005, 16:50:19; Search time 332 Seconds (without alignments) 3163.062 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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162
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5454, Ap Sequence 2123, Ap Sequence 3105, Ap Sequence 262, App Sequence 97, Appl Sequence 72, Appl Sequence 72, Appl
SUMMARIES	9 US-09-864-761-5454 14 US-10-060-036-2123 14 US-10-060-036-3105 19 US-10-717-597-262 19 US-10-283-975A-97 9 US-09-777-430A-72
DB	944 91 91 91 92 91
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% Query Match	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Score	157 157 157 157 157 157 157
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Sequence 104, App Sequence 66, Appl Sequence 1344, Ap Sequence 58, Appl Sequence 17, Appl Sequence 17, Appl Sequence 46, Appl	equence 540, equence 640, equence 640, equence 640, equence 840, equence 950, equence 210, equence 210, equence 310, equen	Sequence 583, App Sequence 211, App Sequence 182, App Sequence 106, App Sequence 106, App Sequence 105, App Sequence 105, App Sequence 105, App Sequence 2, Appli Sequence 4, Appli Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl
19 US-10-776-827-104 16 US-10-210-120-66 18 US-10-641-643-134 19 US-10-283-975A-58 19 US-10-764-649-17 19 US-10-445-990-3	1 US-10-852 2 US-10-852 2 US-10-909 3 US-10-170 3 US-10-170 3 US-10-278 8 US-10-641 1 US-10-671 8 US-10-671 8 US-10-685 6 US-10-685 6 US-10-685 6 US-10-685 7 US-10-339 9 US-10-339 9 US-10-339 9 US-10-339 10-330 10-330	16 US-10-04-090-583 16 US-10-133-013-211 14 US-10-138-846-8922 16 US-10-24'-671-41 10 US-09-981-876-106 9 US-09-148-545-105 22 US-10-138-56-2 19 US-10-833-56-2 19 US-10-833-56-3 19 US-10-833-76 9 US-09-732-793A-54 17 US-10-372-209A-54 17 US-10-372-209A-54
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## ALIGNMENTS

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US-09-664-761-5454/c

Sequence 5454, Application US/09864761

Sequence 5454, Application US/09864761

Sequence 5454, Application US/09864761

GENERAL INCORDANTION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES US CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PLILNG DATE: 2000-09-27

PRIOR PLILNG DATE: 2000-09-27

PRIOR PLILNG DATE: 2000-09-27

PRIOR PLILNG DATE: 2000-09-27

PRIOR PLILNG DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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PRIOR FILING DATE: POT/USO1/00664

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RESULT 4
US-10-717-597-262
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| US-10-060-036-2123 |
| Sequence 2123, Application US/10060036 |
| Publication No. US20030073144A1 |
| GENERAL INFORMATION: |
| APPLICANT: Benson, Darin R. |
| APPLICANT: Lodes, Michael D. |
| APPLICANT: Persing, Michael D. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: William T. |
| APPLICANT: Viang, Yuqiu |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| FILE REFERENCE: 210.12.1.566 |
| CURRENT APPLICATION NUMBER: US/10/060,036 |
| CURRENT FILING DATE: 2002-01.30 |
| NUMBER OF SEQ ID NOS: 4560 |
| SOFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 49117
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SEQ ID NOS: 4944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-5454
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                                                                                                                                                                                                                          195 citchagaccattgrggccaaggagatcrgrgccrgagcagagagagggrtcagga
                                                                                                                                                                                     1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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Sequence 3105, Application US/10060036

Sequence 3105, Application No. US2030073144A1

GENERAL INFORMATION:

APPLICANT: Beneon, Darin R.

APPLICANT: Lodes, Michael D.

APPLICANT: Lodes, Michael J.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Jiang, Yuqiu

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 157; DB 14; Length 475;
Pred. No. 1.8;
                                                                                                   DB 14; Length 473;
1.8;
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                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                          315 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.9%; Score .. 1.8; 68.2%; Pred. No. 1.8; ...tive 50; Mismatches
                                                                                                   Query Match 96.9%; Score 157; DB Best Local Similarity 68.2%; Pred. No. 1.8; Matches 107; Conservative 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 262, Application US/10717597; Publication No. US20040110221A1; GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Burczynski, Michael B.; APPLICANT: Twine, Natalie C.; APPLICANT: Dorner, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.2%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-060-036-3105
LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2123
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WESULT 7
US-10-875-094-72
US-10-875-094-72

Sequence 72, Application US/10875094

Publication No. US20050130179A1

GENERAL INFORMATION.

APPLICANT: Lyamichev, Victor

APPLICANT: Alawi, Hatim T.

APPLICANT: Alawi, Hatim T.

APPLICANT: Takova, Tsetska

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Jeff G.

TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules

CURRENT APPLICATION NORIBER: US/10/875,094

CURRENT APPLICATION NORIBER: US/10/875,094

CURRENT APPLICATION NORIBER: US/10/875,094

CURRENT APPLICATION NORIBER: US/10/875,094

CURRENT APPLICANT: Alawin Norigion 3.2

SEQ ID NO 72

LENGTH: 647
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                                                                                                                                                                    RESULT 6
US-09-777-430A-72
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                    APPLICANT: Slorim, Donna K.
APPLICANT: Slorim, Donna K.
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
FILE REFERENCE: AM101080L
CURRENT PEPLICATION NUMBER: US,10/717,597
CURRENT FILING DATE: 2003-11-21
PRIOR PELICATION NUMBER: US 60/459,782
PRIOR PELICATION NUMBER: US 60/427,982
PRIOR FILING DATE: 2003-14-21
NUMBER OF SEQ ID NOS: 4904
SCOTTAMER PATENTING UPTER: 2002-11-21
NUMBER OF SEQ ID NOS: 4904
SCOTTAMER PATENTING DATE: 2002-11-21
SEQ ID NO 262
LENGTH. 478
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; Publication No. US20040110792A1
; Publication No. US20040110792A1
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 FCT
; CURRENT APPLICATION NUMBER: US/10/283, 975A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340, 938
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
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; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
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96.9%; Score 157; DB 19; Length 478;
Best Local Similarity 68.2%; Pred. No. 1.8;
Matches 107; Conservative 50; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-717-597-262
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APPLICANT:
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Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Patent No. US20020128465A1
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor
APPLICANT: Allawi, Hatim T.
APPLICANT: Allawi, Hatim T.
APPLICANT: Takova, Tsetska
APPLICANT: Nair, Bruce P.
APPLICANT: Nair, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: FORS-04912
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 72
LENGTH: 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTTCAGGA
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                         126 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 162
315 ACCCAAGAAUCUGCAGCUAACUUAUUUCCCCUAGCU 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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Jeffrey J. Seilhamer
Jeffrey J. Schoolstrion FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                Length 725;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WORD PETFECT 6.1 for Windows/MS-DOS 6.2
SOSTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
FLIANG DATE: 14-Aug-2003
FLIANG PATE: APPLICATION: AUKNOWN>
APPLICATION DATA:
APPLICATION NUMBER: AUKNOWN>
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                      Score 157; DB 16;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US
                                                                                                                                                                                                                                                              50; Mismatches
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                    60/334,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1344, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION: GOCKS, Benjamin G. APPLICANT: Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845-4166
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1344:
SEQUENCE CHARACTERISTICS:
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60.
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 66
LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                      96.9%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-210-120-66
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-641-643-1344
                                                                                                                                                                                                                                                            Matches 107;
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                                                                                                                                             TYPE: DNA
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Best Local
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Publication No. US20040132086A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/10/776,827
CURRENT PILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/214,915
PRIOR FILING DATE: 2000-06-28
FRIDR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 Triccarigeaccaccrigeacaaecaaaccaaacriccaaearrigaacacrcacrcacaa 345
                                                                                                                                               1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                           Query Match 96.9%; Score 157; DB 22; Length 647; Best Local Similarity 55.4%; Pred. No. 1.9; Matches 87; Conservative 70; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 661;
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Publication No. US20030175736A1
Publication No. US20030175736A1
APPLICANT: INFORMATION: Arul M.
APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer FILE REFERENCE: UM-07221
CURRENT FAPILCATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 ACCCAAGAATCIGCAGCTAACTIATTITCCCCTAGCT 382
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                                                                                                                                                                                                                                                                                       315 ACCCAAGAAUCUGCAGCUAACUUAUUUCCCCUAGCU 351
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US-10-776-827-104
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        US-10-875-094-72
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LENGTH: 661
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APPLICANT: Devico, Anthony L.
APPLICANT: Garzino, Alfedo
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE OF INVENTION: IMMUNOR 108/10/445,790
CURRENT APPLICATION NUMBER: US/10/445,790
CURRENT FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 09/591,992
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 1997-12-11
    INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 TICCATGGACCACCIGGACAAGCAAACCCAAACTCCGAAGACTIGAACACCTCACTCCACA 367
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 725;
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Best Local Similarity 68.2%; Pred. No. 1.9;
Matches 107; Conservative 50; Mismatches 0;
TITLE OF INVENTION: INFLAMMATORY PROTEINS IN TITLE OF INVENTION: METABOLIC DISORDERS FILE REFERENCE: MPISON3-025PRINM; CURRENT APPLICATION NUMBER: US/10/764,649; CURRENT FILING DATE: 2004-01-26; PRIOR APPLICATION NUMBER: 60/446041; PRIOR FILING DATE: 2003-02-07; WINDER OF SEQ ID NOS: 20 SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/10445790
; Publication No. US20040197305A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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Best Local Similarity 68.2%
Matches 107; Conservative
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; ORGANISM: Homo sapiens
US-10-445-790-3
                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (54)...(353)
US-10-764-649-17
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: human
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Fublication No. US20040110792A1

GENERAL INFORMATION:

APPLICANT: Ortho-Clinical Diagnostics, Inc.

TITLE OF INVENTION: Methods For Assessing and Treating Leukemia FILE REFERENCE: CDS 293 PCT

CURRENT APPLICATION NUMBER: US/10/283, 975A

CURRENT FILING DATE: 2002-10-30

PRIOR FILING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 725
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                                                                                         Query Match 96.9%; Score 157; DB 18; Length 725; Best Local Similarity 68.2%; Pred. No. 1.9; Matches 107; Conservative 50; Mismatches 0; Indels
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Publication No. US20040157253A1
GENERAL INFORMATION:
APPLICANT: Xu, Haiyan
APPLICANT: Chon, Hong
APPLICANT: Barnes, Glenn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
                                                                                                                                                                                                                                                                                                                                                     368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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  CLONE: 934513
SEQUENCE DESCRIPTION: SEQ ID NO: 1344:
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Best Local Similarity 68.2*
Matches 107; Conservative
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ORGANISM: HUMAN
                                             US-10-641-643-1344
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// Sequence 46, Application US/10852335A

// Sequence 46, Application US/10852335A

// Sequence 46, Application US/10852335A

// Sequence 46, Application US/10852335A

// SENERAL INFORMATION: USO050112129A1

// APPLICANT: HEIDI S. PHILLIPS

// TITLE OF INVENTION: Compositions and Methods for the Diagnosis and

// TITLE OF INVENTION: Treatment of Tumors of Glial Origin

// TITLE OF INVENTION: Treatment of Tumors of Glial Origin

// TITLE OF INVENTION: Treatment of Tumors of Glial Origin

// TITLE OF INVENTION: 2004-05-24

// PRIOR PILLING DATE: 2004-05-24

// PRIOR FILLING DATE: 2004-02-27

// PRIOR FILLING DATE: 2003-05-23

// NUMBER OF SEQ ID NOS: 190

// SEQ ID NO 46

// IENGTH: 725
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US-10-852-335A-54
; Sequence 54, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; CURRENT APPLICATION NUMBER: US/10/852,335A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/473,238
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              368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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SEQ ID NO 54
LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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